



SEQUENCE LISTING

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<120> METHODS AND MICROORGANISMS FOR PRODUCTION OF
 PANTO-COMPOUNDS

<130> BGI-141CP

<140> USSN 09/667,569
 <141> 2000-09-21

<150> USSN 09/400,494
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<150> USSN 60/210,072
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<150> USSN 60/227,860
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<170> PatentIn. Ver. 2.0

<210> 1
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 <213> Haemophilus influenzae

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 Gln Trp Ala Glu Leu Arg Lys Ser Val Pro Leu Lys Leu Thr Glu Gln
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 Asp Leu Lys Pro Leu Leu Gly Phe Asn Glu Asp Leu Ser Leu Asp Glu
 35 40 45
 Val Ser Thr Ile Tyr Leu Pro Leu Thr Arg Leu Ile Asn Tyr Tyr Ile
 50 55 60
 Asp Glu Asn Leu His Arg Gln Thr Val Leu His Arg Phe Leu Gly Arg
 65 70 75 80
 Asn Asn Ala Lys Thr Pro Tyr Ile Ile Ser Ile Ala Gly Ser Val Ala
 85 90 95
 Val Gly Lys Ser Thr Ser Ala Arg Ile Leu Gln Ser Leu Leu Ser His
 100 105 110
 Trp Pro Thr Glu Arg Lys Val Asp Leu Ile Thr Thr Asp Gly Phe Leu
 115 120 125

Tyr Pro Leu Asn Lys Leu Lys Gln Asp Asn Leu Leu Gln Lys Lys Gly
 130 135 140
 Phe Pro Val Ser Tyr Asp Thr Pro Lys Leu Ile Arg Phe Leu Ala Asp
 145 150 155 160
 Val Lys Ser Gly Lys Ser Asn Val Thr Ala Pro Ile Tyr Ser His Leu
 165 170 175
 Thr Tyr Asp Ile Ile Pro Asp Lys Phe Asp Val Val Asp Lys Pro Asp
 180 185 190
 Ile Leu Ile Leu Glu Gly Leu Asn Val Leu Gln Thr Gly Asn Asn Lys
 195 200 205
 Thr Asp Gln Thr Phe Val Ser Asp Phe Val Asp Phe Ser Ile Tyr Val
 210 215 220
 Asp Ala Glu Glu Lys Leu Leu Lys Glu Trp Tyr Ile Lys Arg Phe Leu
 225 230 235 240
 Lys Phe Arg Glu Ser Ala Phe Asn Asp Pro Asn Ser Tyr Phe Lys His
 245 250 255
 Tyr Ala Ser Leu Ser Lys Glu Glu Ala Ile Ala Thr Ala Ser Lys Ile
 260 265 270
 Trp Asp Glu Ile Asn Gly Leu Asn Leu Asn Gln Asn Ile Leu Pro Thr
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 Arg Glu Arg Ala Asn Leu Ile Leu Lys Lys Gly His Asn His Gln Val
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 Glu Leu Ile Lys Leu Arg Lys
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 <213> Escherichia coli

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 Glu Asp Glu Ile Ala Arg Leu Lys Gly Ile Asn Glu Asp Leu Ser Leu
 35 40 45
 Glu Glu Val Ala Glu Ile Tyr Leu Pro Leu Ser Arg Leu Leu Asn Phe
 50 55 60
 Tyr Ile Ser Ser Asn Leu Arg Arg Gln Ala Val Leu His Ala Phe Leu
 65 70 75
 Gly Thr Asn Gly Gln Arg Ile Pro Tyr Ile Ile Ser Ile Ala Gly Ser
 80 85 90

Val Ala Val Gly Lys Ser Thr Thr Ala Arg Val Leu Gln Ala Leu Leu
100 105 110

Ser Arg Trp Pro Glu His Arg Arg Val Glu Leu Ile Thr Thr Asp Gly
115 120 125

Phe Leu His Pro Asn Gln Val Leu Lys Glu Arg Gly Leu Met Lys Lys
130 135 140

Lys Gly Phe Pro Glu Ser Tyr Asp Met His Arg Leu Val Lys Phe Val
145 150 155 160

Ser Asp Leu Lys Ser Gly Val Pro Asn Val Thr Ala Pro Val Tyr Ser
165 170 175

His Leu Ile Tyr Asp Val Ile Pro Asp Gly Asp Lys Thr Val Val Gln
180 185 190

Pro Asp Ile Leu Ile Leu Glu Gly Leu Asn Val Leu Gln Ser Gly Met
195 200 205

Asp Tyr Pro His Asp Pro His His Val Phe Val Ser Asp Phe Val Asp
210 215 220

Phe Ser Ile Tyr Val Asp Ala Pro Glu Asp Leu Leu Gln Thr Trp Tyr
225 230 235 240

Ile Asn Arg Phe Leu Lys Phe Arg Glu Gly Ala Phe Thr Asp Pro Asp
245 250 255

Ser Tyr Phe His Asn Tyr Ala Lys Leu Thr Lys Glu Glu Ala Ile Lys
260 265 270

Thr Ala Met Thr Leu Trp Lys Glu Ile Asn Trp Leu Asn Leu Lys Gln
275 280 285

Asn Ile Leu Pro Thr Arg Glu Arg Ala Ser Leu Ile Leu Thr Lys Ser
290 295 300

Ala Asn His Ala Val Glu Glu Val Arg Leu Arg Lys
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<213> Bacillus subtilis

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Met Lys Asn Lys Glu Leu Asn Leu His Thr Leu Tyr Thr Gln His Asn
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Arg Glu Ser Trp Ser Gly Phe Gly Gly His Leu Ser Ile Ala Val Ser
20 25 30 35

His Glu Glu Ala Lys Ala Val Glu Gly Leu Asn Asp Tyr Leu Ser Val
40 45 50 55

His Val Val Glu Thr Ile Tyr Ile Pro Leu Val Arg Ile Leu His Leu
60 65 70 75

His Val Lys Ser Ala Ala Glu Arg Asn Lys His Val Asn Val Phe Leu
 65 70 75 80
 Lys His Pro His Ser Ala Lys Ile Pro Phe Ile Ile Gly Ile Ala Gly
 85 90 95
 Ser Val Ala Val Gly Lys Ser Thr Thr Ala Arg Ile Leu Gln Lys Leu
 100 105 110
 Leu Ser Arg Leu Pro Asp Arg Pro Lys Val Ser Leu Ile Thr Thr Asp
 115 120 125
 Gly Phe Leu Phe Pro Thr Ala Glu Leu Lys Lys Lys Asn Met Met Ser
 130 135 140
 Arg Lys Gly Phe Pro Glu Ser Tyr Asp Val Lys Ala Leu Leu Glu Phe
 145 150 155 160
 Leu Asn Asp Leu Lys Ser Gly Lys Asp Ser Val Lys Ala Pro Val Tyr
 165 170 175
 Ser His Leu Thr Tyr Asp Arg Glu Glu Gly Val Phe Glu Val Val Glu
 180 185 190
 Gln Ala Asp Ile Val Ile Ile Glu Gly Ile Asn Val Leu Gln Ser Pro
 195 200 205
 Thr Leu Glu Asp Asp Arg Glu Asn Pro Arg Ile Phe Val Ser Asp Phe
 210 215 220
 Phe Asp Phe Ser Ile Tyr Val Asp Ala Glu Glu Ser Arg Ile Phe Thr
 225 230 235 240
 Trp Tyr Leu Glu Arg Phe Arg Leu Leu Arg Glu Thr Ala Phe Gln Asn
 245 250 255
 Pro Asp Ser Tyr Phe His Lys Phe Lys Asp Leu Ser Asp Gln Glu Ala
 260 265 270
 Asp Glu Met Ala Ala Ser Ile Trp Glu Ser Val Asn Arg Pro Asn Leu
 275 280 285
 Tyr Glu Asn Ile Leu Pro Thr Lys Phe Arg Ser Asp Leu Ile Leu Arg
 290 295 300
 Lys Gly Asp Gly His Lys Val Glu Glu Val Leu Val Arg Arg Val
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<210> 4

<211> 312

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<213> Mycobacterium leprae

<400> 4

Met His Arg Leu Ser Glu Pro Ser Pro Tyr Val Glu Phe Asp Arg Lys
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His Trp Arg Ala Leu Arg Met Ser Thr Pro Leu Ala Leu Thr Glu Glu
 31 41 51 61 71

Glu Leu Ile Gly Leu Arg Gly Leu Gly Glu Gln Ile Asp Leu Leu Glu
 35 40 45
 Val Glu Glu Val Tyr Leu Pro Leu Ala Arg Leu Ile His Leu Gln Val
 50 55 60
 Ala Ala Arg Gln Arg Leu Phe Ala Ala Thr Ala Glu Phe Leu Gly Glu
 65 70 75 80
 Pro Gln Gln Asn Pro Gly Arg Pro Val Pro Phe Ile Ile Gly Val Ala
 85 90 95
 Gly Ser Val Ala Val Gly Lys Ser Thr Thr Ala Arg Val Leu Gln Ala
 100 105 110
 Leu Leu Ala Arg Trp Asp His His Thr Arg Val Asp Leu Val Thr Thr
 115 120 125
 Asp Gly Phe Leu Tyr Pro Asn Ala Glu Leu Gly Arg Arg Asn Leu Met
 130 135 140
 His Arg Lys Gly Phe Pro Glu Ser Tyr Asn Arg Arg Ala Leu Met Arg
 145 150 155 160
 Phe Val Thr Ser Val Lys Ser Gly Ala Asp Tyr Ala Cys Ala Pro Val
 165 170 175
 Tyr Ser His Leu Arg Tyr Asp Thr Ile Pro Gly Ala Lys His Val Val
 180 185 190
 Arg His Pro Asp Ile Leu Ile Leu Glu Gly Leu Asn Val Leu Gln Thr
 195 200 205
 Gly Pro Thr Leu Met Val Ser Asp Leu Phe Asp Phe Ser Leu Tyr Val
 210 215 220
 Asp Ala Arg Ile Gln Asp Ile Glu Gln Trp Tyr Val Ser Arg Phe Leu
 225 230 235 240
 Ala Met Arg Gly Thr Ala Phe Ala Asp Pro Glu Ser His Phe His His
 245 250 255
 Tyr Ser Ala Leu Thr Asp Ser Lys Ala Ile Ile Ala Ala Arg Glu Ile
 260 265 270
 Trp Arg Ser Ile Asn Arg Pro Asn Leu Val Glu Asn Ile Leu Pro Thr
 275 280 285
 Arg Pro Arg Ala Thr Leu Val Leu Arg Lys Asp Ala Asp His Ser Ile
 290 295 300
 Asp Arg Leu Arg Leu Arg Lys Leu
 305 310

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Met	Ser	Arg	Leu	Ser	Glu	Pro	Ser	Pro	Tyr	Val	Glu	Phe	Asp	Arg	Arg	1	5	10	15
Gln	Trp	Arg	Ala	Leu	Arg	Met	Ser	Thr	Pro	Leu	Ala	Leu	Thr	Glu	Glu	20	25	30	
Glu	Leu	Val	Gly	Leu	Arg	Gly	Leu	Gly	Glu	Gln	Ile	Asp	Leu	Leu	Glu	35	40	45	
Val	Glu	Glu	Val	Tyr	Leu	Pro	Leu	Ala	Arg	Leu	Ile	His	Leu	Gln	Val	50	55	60	
Ala	Ala	Arg	Gln	Arg	Leu	Phe	Ala	Ala	Thr	Ala	Glu	Phe	Leu	Gly	Glu	65	70	75	80
Pro	Gln	Gln	Asn	Pro	Asp	Arg	Pro	Val	Pro	Phe	Ile	Ile	Gly	Val	Ala	85	90	95	
Gly	Ser	Val	Ala	Val	Gly	Lys	Ser	Thr	Thr	Ala	Arg	Val	Leu	Gln	Ala	100	105	110	
Leu	Leu	Ala	Arg	Trp	Asp	His	His	Pro	Arg	Val	Asp	Leu	Val	Thr	Thr	115	120	125	
Asp	Gly	Phe	Leu	Tyr	Pro	Asn	Ala	Glu	Leu	Gln	Arg	Arg	Asn	Leu	Met	130	135	140	
His	Arg	Lys	Gly	Phe	Pro	Glu	Ser	Tyr	Asn	Arg	Arg	Ala	Leu	Met	Arg	145	150	155	160
Phe	Val	Thr	Ser	Val	Lys	Ser	Gly	Ser	Asp	Tyr	Ala	Cys	Ala	Pro	Val	165	170	175	
Tyr	Ser	His	Leu	His	Tyr	Asp	Ile	Ile	Pro	Gly	Ala	Glu	Gln	Val	Val	180	185	190	
Arg	His	Pro	Asp	Ile	Leu	Ile	Leu	Glu	Gly	Leu	Asn	Val	Leu	Gln	Thr	195	200	205	
Gly	Pro	Thr	Leu	Met	Val	Ser	Asp	Leu	Phe	Asp	Phe	Ser	Leu	Tyr	Val	210	215	220	
Asp	Ala	Arg	Ile	Glu	Asp	Ile	Glu	Gln	Trp	Tyr	Val	Ser	Arg	Phe	Leu	225	230	235	240
Ala	Met	Arg	Thr	Thr	Ala	Phe	Ala	Asp	Pro	Glu	Ser	His	Phe	His	His	245	250	255	
Tyr	Ala	Ala	Phe	Ser	Asp	Ser	Gln	Ala	Val	Val	Ala	Ala	Arg	Glu	Ile	260	265	270	
Trp	Arg	Thr	Ile	Asn	Arg	Pro	Asn	Leu	Val	Glu	Asn	Ile	Leu	Pro	Thr	275	280	285	
Arg	Pro	Arg	Ala	Thr	Leu	Val	Leu	Arg	Lys	Asp	Ala	Asp	His	Ser	Ile	290	295	300	
Asn	Arg	Leu	Arg	Leu	Arg	Lys	Leu									305	310		

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Pro Glu Ala Thr Pro Tyr Val Asp Leu Thr Arg Pro Glu Trp Ser Ala
10 25 30

[illegible]

Leu Arg Gly Leu Gly Asp Val Ile Asp Leu Asp Glu Val Arg Asp Ile
50 55 60

Tyr Leu Pro Leu Ser Arg Leu Leu Asn Leu Tyr Val Gly Ala Thr Asp
65 70 75 80

Gly Leu Arg Gly Ala Leu Asn Thr Phe Leu Gly Glu Gln Gly Ser Gln
90 90 90

Ser Gly Thr Pro Phe Val Ile Gly Val Ala Gly Ser Val Ala Val Gly
100 105 110

Lys Ser Thr Val Ala Arg Leu Leu Gln Ala Leu Leu Ser Arg Trp Pro
115 120 125

[illegible]

Thr Arg Glu Leu His Ala Arg Gly Leu Met Ser Arg Lys Gly Ihe Pro
146 150 154 160

Glu Ser Tyr Asp Arg Arg Ala Leu Thr Arg Phe Val Ala Asp Ile Lys
165 170 175

$$\frac{1}{\sqrt{2}} \begin{pmatrix} 1 & 0 \\ 0 & 1 \end{pmatrix}, \frac{1}{\sqrt{2}} \begin{pmatrix} 1 & 0 \\ 0 & -1 \end{pmatrix}, \frac{1}{\sqrt{2}} \begin{pmatrix} 0 & 1 \\ 1 & 0 \end{pmatrix}, \frac{1}{\sqrt{2}} \begin{pmatrix} 0 & -i \\ i & 0 \end{pmatrix}, \frac{1}{\sqrt{2}} \begin{pmatrix} 1 & i \\ 0 & 0 \end{pmatrix}, \frac{1}{\sqrt{2}} \begin{pmatrix} 1 & -i \\ 0 & 0 \end{pmatrix}, \frac{1}{\sqrt{2}} \begin{pmatrix} 0 & 1 \\ -1 & 0 \end{pmatrix}, \frac{1}{\sqrt{2}} \begin{pmatrix} 0 & i \\ 1 & 0 \end{pmatrix}, \frac{1}{\sqrt{2}} \begin{pmatrix} 0 & -1 \\ 1 & 0 \end{pmatrix}, \frac{1}{\sqrt{2}} \begin{pmatrix} 0 & -i \\ 1 & 0 \end{pmatrix}, \frac{1}{\sqrt{2}} \begin{pmatrix} 1 & 0 \\ 0 & 0 \end{pmatrix}, \frac{1}{\sqrt{2}} \begin{pmatrix} 1 & 0 \\ 0 & 0 \end{pmatrix}, \frac{1}{\sqrt{2}} \begin{pmatrix} 0 & 1 \\ 0 & 0 \end{pmatrix}, \frac{1}{\sqrt{2}} \begin{pmatrix} 0 & -1 \\ 0 & 0 \end{pmatrix}, \frac{1}{\sqrt{2}} \begin{pmatrix} 0 & 0 \\ 1 & 0 \end{pmatrix}, \frac{1}{\sqrt{2}} \begin{pmatrix} 0 & 0 \\ -1 & 0 \end{pmatrix}, \frac{1}{\sqrt{2}} \begin{pmatrix} 0 & 0 \\ 0 & 1 \end{pmatrix}, \frac{1}{\sqrt{2}} \begin{pmatrix} 0 & 0 \\ 0 & -1 \end{pmatrix}$$

Asp Ile Val Pro Asp Gln Arg Leu Val Val Arg Arg Pro Asp Ile Leu
195 200 205

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	5
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60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100

[illegible]

Any type I can Any All The All The All None Of Any One Type Two Any
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[illegible]

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Thr Arg Gly Arg Ala Thr Leu Val Leu Arg Lys Gly Pro Asp His Lys
305 310 315 320

Val Gln Arg Leu Ser Leu Arg Lys Leu
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<210> 7

<211> 265

<212> PRT

<213> Streptomyces coelicolor

<400> 7

Met Leu Leu Thr Ile Asp Val Gly Asn Thr His Thr Val Leu Gly Leu
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Phe Asp Gly Glu Asp Ile Val Glu His Trp Arg Ile Ser Thr Asp Ser
20 25 30

Arg Arg Thr Ala Asp Glu Leu Ala Val Leu Leu Gln Gly Leu Met Gly
35 40 45

Met His Pro Leu Leu Gly Asp Glu Leu Gly Asp Gly Ile Asp Gly Ile
50 55 60

Ala Ile Cys Ala Thr Val Pro Ser Val Leu His Glu Leu Arg Glu Val
65 70 75 80

Thr Arg Arg Tyr Tyr Gly Asp Val Pro Ala Val Leu Val Glu Pro Gly
85 90 95

Val Lys Thr Gly Val Pro Ile Leu Thr Asp His Pro Lys Glu Val Gly
100 105 110

Ala Asp Arg Ile Ile Asn Ala Val Ala Ala Val Glu Leu Tyr Gly Gly
115 120 125

Pro Ala Ile Val Val Asp Phe Gly Thr Ala Thr Thr Phe Asp Ala Val
130 135 140

Ser Ala Arg Gly Glu Tyr Ile Gly Gly Val Ile Ala Pro Gly Ile Glu
145 150 155 160

Ile Ser Val Glu Ala Leu Gly Val Lys Gly Ala Gln Leu Arg Lys Ile
165 170 175

Glu Val Ala Arg Pro Arg Ser Val Ile Gly Lys Asn Thr Val Glu Ala
180 185 190

Met Gln Ser Gly Ile Val Tyr Gly Phe Ala Gly Gln Val Asp Gly Val
195 200 205

Val Asn Arg Met Ala Arg Gln Leu Ala Asp Asp Pro Asp Asp Val Thr
210 215 220

Val Ile Ala Thr Gly Gly Leu Ala Pro Met Val Leu Gly Gln Ser Ser
225 230 235 240

Val Ile Asp Gln His Gln Pro Trp Leu Thr Leu Met Gly Leu Arg Leu

245

250

255

Val Tyr Glu Arg Asn Val Ser Arg Met
260 265

<210> 8

<211> 272

<212> PRT

<213> Mycobacterium tuberculosis

<400> 8

Met Leu Leu Ala Ile Asp Val Arg Asn Thr His Thr Val Val Gly Leu
1 5 10 15

Leu Ser Gly Met Lys Glu His Ala Lys Val Val Gln Gln Trp Arg Ile
20 25 30

Arg Thr Glu Ser Glu Val Thr Ala Asp Glu Leu Ala Leu Thr Ile Asp
35 40 45

Gly Leu Ile Gly Glu Asp Ser Glu Arg Leu Thr Gly Thr Ala Ala Leu
50 55 60

Ser Thr Val Pro Ser Val Leu His Glu Val Arg Ile Met Leu Asp Gln
65 70 75 80

Tyr Trp Pro Ser Val Pro His Val Leu Ile Glu Pro Gly Val Arg Thr
85 90 95

Gly Ile Pro Leu Leu Val Asp Asn Pro Lys Glu Val Gly Ala Asp Arg
100 105 110

Ile Val Asn Cys Leu Ala Ala Tyr Asp Arg Phe Arg Lys Ala Ala Ile
115 120 125

Val Val Asp Phe Gly Ser Ser Ile Cys Val Asp Val Val Ser Ala Lys
130 135 140

Gly Glu Phe Leu Gly Gly Ala Ile Ala Pro Gly Val Gln Val Ser Ser
145 150 155 160

Asp Ala Ala Ala Ala Arg Ser Ala Ala Leu Arg Arg Val Glu Leu Ala
165 170 175

Arg Pro Arg Ser Val Val Gly Lys Asn Thr Val Gln Cys Met Gln Ala
180 185 190

Gly Ala Val Phe Gly Phe Ala Gly Leu Val Asp Gly Leu Val Gly Arg
195 200 205

Ile Arg Glu Asp Val Ser Gly Phe Ser Val Asp His Asp Val Ala Ile
210 215 220

Val Ala Thr Gly His Thr Ala Fr Leu Leu Leu Pro Gln Leu His Thr
225 230 235 240

Val Asp His Tyr Asp Gln His Leu Thr Leu Gln Gly Leu Arg Leu Val
245 250 255

Phe Gln Arg Asn Leu Gln Val Gln Arg Gly Arg Leu Lys Thr Ala Arg

160

165

270

<211> 9
 <211> 258
 <212> PRT
 <213> *Bacillus subtilis*

<400> 9

Leu Leu Leu Val Ile Asp Val Gly Asn Thr Asn Thr Val Leu Gly Val
 1 5 10 15

Tyr His Asp Gly Lys Leu Glu Tyr His Trp Arg Ile Glu Thr Ser Arg
 20 25 30

His Lys Thr Glu Asp Glu Phe Gly Met Ile Leu Arg Ser Leu Phe Asp
 35 40 45

His Ser Gly Leu Met Phe Glu Gln Ile Asp Gly Ile Ile Ile Ser Ser
 50 55 60

Val Val Pro Pro Ile Met Phe Ala Leu Glu Arg Met Cys Thr Lys Tyr
 65 70 75 80

Phe His Ile Glu Pro Gln Ile Val Gly Pro Gly Met Lys Thr Gly Leu
 85 90 95

Asn Ile Lys Tyr Asp Asn Pro Lys Glu Val Gly Ala Asp Arg Ile Val
 100 105 110

Asn Ala Val Ala Ala Ile His Leu Tyr Gly Asn Pro Leu Ile Val Val
 115 120 125

Asp Phe Gly Thr Ala Thr Thr Tyr Cys Tyr Ile Asp Glu Asn Lys Gln
 130 135 140

Tyr Met Gly Gly Ala Ile Ala Pro Gly Ile Thr Ile Ser Thr Glu Ala
 145 150 155 160

Leu Tyr Ser Arg Ala Ala Lys Leu Pro Arg Ile Glu Ile Thr Arg Pro
 165 170 175

Asp Asn Ile Ile Gly Lys Asn Thr Val Ser Ala Met Gln Ser Gly Ile
 180 185 190

Leu Phe Gly Tyr Val Gly Gln Val Glu Gly Ile Val Lys Arg Met Lys
 195 200 205

Trp Glu Ala Lys Gln Asp Leu Lys Val Ile Ala Thr Gly Gly Leu Ala
 210 215 220

Pro Leu Ile Ala Asn Gln Ser Asp Lys Ile Asp Ile Val Asp Pro Phe
 225 230 235 240

Leu Thr Leu Lys Gly Leu Gln Leu Ile Tyr Glu Arg Asn Arg Val Gly
 245 250 255

Ser Val

<210> 10
 <211> 262
 <212> FRT
 <213> *Deinococcus radiopugnans*

<400> 10
 Met Pro Ala Phe Pro Leu Leu Ala Val Asp Ile Gly Asn Thr Thr Thr
 1 5 10 15
 Val Leu Gly Leu Ala Asp Ala Ser Gly Ala Leu Thr His Thr Trp Arg
 20 25 30
 Ile Arg Thr Asn Arg Glu Met Leu Pro Asp Asp Leu Ala Leu Gln Leu
 35 40 45
 His Gly Leu Phe Thr Leu Ala Gly Ala Pro Ile Pro Arg Ala Ala Val
 50 55 60
 Leu Ser Ser Val Ala Pro Pro Val Gly Glu Asn Tyr Ala Leu Ala Leu
 65 70 75 80
 Lys Arg His Phe Met Ile Asp Ala Phe Ala Val Ser Ala Glu Asn Leu
 85 90 95
 Pro Asp Val Thr Val Glu Leu Asp Thr Pro Gly Ser Val Gly Ala Asp
 100 105 110
 Arg Leu Cys Asn Leu Phe Gly Ala Glu Lys Tyr Leu Gly Gly Leu Asp
 115 120 125
 Tyr Ala Val Val Val Asp Phe Gly Thr Ser Thr Asn Phe Asp Val Val
 130 135 140
 Gly Arg Gly Arg Arg Phe Leu Gly Gly Ile Leu Ala Thr Gly Ala Gln
 145 150 155 160
 Val Ser Ala Asp Ala Leu Phe Ala Arg Ala Ala Lys Leu Pro Arg Ile
 165 170 175
 Thr Leu Gln Ala Pro Glu Thr Ala Ile Gly Lys Asn Thr Val His Ala
 180 185 190
 Leu Gln Ser Gly Leu Val Phe Gly Tyr Ala Glu Met Val Asp Gly Leu
 195 200 205
 Leu Arg Arg Ile Arg Ala Glu Leu Pro Gly Glu Ala Val Ala Val Ala
 210 215 220
 Thr Gly Gly Phe Ser Arg Thr Val Glu Gly Ile Lys Gln Glu Ile Asp
 225 230 235 240
 Tyr Tyr Asp Glu Thr Leu Thr Leu Arg Gly Leu Val Glu Leu Trp Ala
 245 250 255
 Ser Arg Ser Glu Val Arg

[illegible]

Phe Gln Thr Val Asp Gln Leu Phe Ser His Leu His Pro Leu Leu Gly
 30 40 48
 Asp Ala Met Arg Glu Ile Lys Gly Ile Gly Val Ala Ser Val Val Pro
 50 58 60
 Thr Gln Asn Thr Val Ile Gln Arg Phe Ser Gln Lys Tyr Phe His Ile
 65 70 75 80
 Ser Pro Ile Trp Val Lys Ala Lys Asn Gly Cys Val Lys Trp Asn Val
 85 90 95
 Lys Asn Pro Ser Glu Val Gly Ala Asp Arg Val Ala Asn Val Val Ala
 100 105 110
 Phe Val Lys Glu Tyr Gly Lys Asn Gly Ile Ile Ile Asp Met Gly Thr
 115 120 125
 Ala Thr Thr Val Asp Leu Val Val Asn Gly Ser Tyr Glu Gly Gly Ala
 130 135 140
 Ile Leu Pro Gly Phe Phe Met Met Val His Ser Leu Phe Arg Gly Thr
 145 150 155 160
 Ala Lys Leu Pro Leu Val Glu Val Lys Pro Ala Asp Phe Val Val Gly
 165 170 175
 Lys Asp Thr Glu Glu Asn Ile Arg Leu Gly Val Val Asn Gly Ser Val
 180 185 190
 Tyr Ala Leu Glu Gly Ile Ile Gly Arg Ile Lys Glu Val Tyr Gly Asp
 195 200 205
 Leu Pro Val Val Leu Thr Gly Gly Gln Ser Lys Ile Val Lys Asp Met
 210 215 220
 Ile Lys His Glu Ile Phe Asp Glu Asp Leu Thr Ile Lys Gly Val Tyr
 225 230 235 240
 His Phe Cys Phe Gly Asp
 245

<210> 13
 <211> 273
 <212> PRT
 <213> Trepanema pallidum

<400> 13
 Met Leu Leu Ile Asp Val Gly Asn Ser His Val Val Phe Gly Ile Gln
 1 2 10 15
 Gly Glu Asn Gly Gly Arg Val Cys Val Arg Glu Leu Phe Arg Leu Ala
 20 25 30
 Pro Asp Ala Arg Lys Thr Gln Asp Glu Tyr Ser Leu Leu Ile His Ala
 35 40 45
 Leu Tyr Glu Arg Ala Gly Val Gly Arg Ala Ser Leu Arg Asp Ala Ile
 50 55 60

Ile Ser Ser Val Val Pro Val Leu Thr Lys Thr Ile Ala Asp Ala Val
 68 71 75 80
 Ala Gln Ile Ser Gly Val Gln Pro Val Val Phe Gly Pro Trp Ala Tyr
 85 90 95
 Glu His Leu Pro Val Arg Ile Pro Glu Pro Val Arg Ala Glu Ile Gly
 100 105 110
 Thr Asp Leu Val Ala Asn Ala Val Ala Ala Tyr Val His Phe Arg Ser
 115 120 125
 Ala Cys Val Val Val Asp Cys Gly Thr Ala Leu Thr Phe Thr Ala Val
 130 135 140
 Asp Gly Thr Gly Leu Ile Gln Gly Val Ala Ile Ala Pro Gly Leu Arg
 145 150 155 160
 Thr Ala Val Gln Ser Leu His Thr Gly Thr Ala Gln Leu Pro Leu Val
 165 170 175
 Pro Leu Ala Leu Pro Asp Ser Val Leu Gly Lys Asp Thr Thr His Ala
 180 185 190
 Val Gln Ala Gly Val Val Arg Gly Thr Leu Phe Val Ile Arg Ala Met
 195 200 205
 Ile Ala Gln Cys Gln Lys Glu Leu Gly Cys Arg Cys Ala Ala Val Ile
 210 215 220
 Thr Gly Gly Leu Ser Arg Leu Phe Ser Ser Glu Val Asp Phe Pro Pro
 225 230 235 240
 Ile Asp Ala Gln Leu Thr Leu Ser Gly Leu Ala His Ile Ala Arg Leu
 245 250 255
 Val Pro Thr Ser Leu Leu Pro Pro Ala Thr Val Ser Gly Ser Ser Gly
 260 265 270

Asn

<110> 14
 <111> 262
 <112> PRT
 <113> Borrelia burgdorferi

<400> 14
 Met Asn Lys Pro Leu Leu Ser Glu Leu Ile Ile Asp Ile Gly Asn Thr
 1 5 10 15
 Ser Ile Ala Phe Ala Leu Phe Lys Asp Asn Gln Val Asn Leu Phe Ile
 20 25 30
 Lys Met Lys Thr Asn Leu Met Leu Ala Tyr Asp Glu Val Tyr Ser Phe
 35 40 45
 Phe Ala Ala Asn Phe Asp Phe Asn Val Asn Lys Val Ile Ile Ser Ser
 50 55 60

Val Val Phe Ile Leu Asn Gln Thr Phe Lys Asn Val Ile Phe Ser Phe
 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99
 Phe Lys Ile Lys Pro Leu Phe Ile Gly Phe Asp Leu Asn Tyr Asp Leu
 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114
 Thr Phe Asn Pro Tyr Lys Ser Asp Lys Phe Leu Leu Gly Ser Asp Val
 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129
 Phe Ala Asn Leu Val Ala Ala Ile Gln Asn Tyr Ser Phe Gln Asn Val
 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144
 Leu Val Val Asp Leu Gly Thr Ala Cys Thr Ile Phe Ala Val Ser Arg
 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159
 Gln Asp Gly Ile Leu Gly Gly Ile Ile Asn Ser Gly Pro Leu Ile Asn
 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174
 Phe Asn Ser Leu Leu Asp Asn Ala Tyr Leu Ile Lys Lys Phe Pro Ile
 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189
 Ser Thr Pro Asn Asn Leu Leu Gln Arg Thr Thr Ser Gly Ser Val Asn
 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204
 Ser Gly Leu Phe Tyr Gln Tyr Lys Tyr Leu Ile Gln Gly Val Tyr Arg
 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219
 Asp Ile Lys Gln Met Tyr Lys Lys Lys Phe Asn Leu Ile Ile Thr Gly
 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234
 Gly Asn Ala Asp Leu Ile Leu Ser Leu Ile Gln Ile Gln Phe Ile Phe
 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249
 Asn Ile His Leu Thr Val Gln Gly Val Arg Ile Leu Gly Asn Ser Ile
 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264
 Asp Phe Lys Phe Val Asn
 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279

<210> 15

<211> 229

<212> FRT

<213> Aquifex aeolicus

<400> 15

Met Arg Phe Leu Thr Val Asp Val Gly Asn Ser Ser Val Asp Ile Ala
 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15
 Leu Trp Gln Gly Lys Lys Val Lys Asp Phe Leu Lys Leu Ser His Gln
 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30
 Gln Phe Leu Lys Gln Gln Phe Pro Lys Leu Lys Ala Leu Gly Ile Ser
 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45
 Val Lys Gln Ser Phe Ser Gln Lys Val Arg Gly Lys Ile Pro Lys Ile
 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60
 Lys Phe Leu Lys Lys Gln Asn Phe Pro Ile Gln Val Asp Tyr Lys Thr
 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75

Ile Thr Gly Phe Asp Gln Asp Lys Lys Leu Val Gly Gly Ala Ile Leu
 131 131 140
 Pro Gly Leu Gly Leu Gln Leu Ala Thr Leu Gly Asp Arg Leu Ala Ala
 145 150 155 160
 Leu Pro Lys Leu Glu Met Asp Gln Leu Thr Glu Leu Pro Asp Arg Trp
 165 170 175
 Ala Leu Asp Thr Pro Ser Ala Ile Phe Ser Gly Val Val Tyr Gly Val
 180 185 190
 Leu Gly Ala Leu Gln Ser Tyr Leu Gln Asp Trp Gln Lys Leu Phe Pro
 195 200 205
 Gly Ala Ala Met Val Ile Thr Gly Gly Asp Gly Lys Ile Leu His Gly
 210 215 220
 Phe Leu Lys Glu His Ser Pro Asn Leu Ser Val Ala Trp Asp Asp Asn
 225 230 235 240
 Leu Ile Phe Leu Gly Met Ala Ala Ile His His Gly Asp Arg Pro Ile
 245 250 255

Cys

<210> 17
 <211> 223
 <212> PRT
 <213> Helicobacter pylori

<400> 17
 Met Phe Ala Arg Gln Ser Phe Thr Asp Leu Lys Asn Leu Val Leu Cys
 1 5 10 15
 Asp Ile Gly Asn Thr Arg Ile His Phe Ala Gln Asn Tyr Gln Leu Phe
 20 25 30
 Ser Ser Ala Lys Glu Asp Leu Lys Arg Leu Gly Ile Gln Lys Glu Ile
 35 40 45
 Phe Tyr Ile Ser Val Asn Glu Glu Asn Glu Lys Ala Leu Leu Asn Cys
 50 55 60
 Tyr Pro Asn Ala Lys Asn Ile Ala Gly Phe Phe His Leu Gln Thr Asp
 65 70 75 80
 Tyr Val Gly Leu Gly Ile Asp Arg Gln Met Ala Cys Leu Ala Val Asn
 85 90 95
 Asn Gly Val Val Val Asp Ala Gly Ser Ala Ile Thr Ile Asp Leu Ile
 100 105 110
 Lys Glu Gly Lys His Leu Gly Gly Cys Ile Leu Phe Gly Leu Ala Asn
 115 120 125
 Tyr Ile His Ala Tyr Lys Lys Ser Ala Lys Ile Leu Gln Glu Phe Phe
 130 135 140 145

Lys Ala Leu Asp Ser Leu Glu Val Leu Pro Lys Ser Thr Arg Asp Ala
 148 150 155 160
 Val Asn Tyr Gly Met Val Leu Ser Val Ile Ala Cys Ile Gln His Leu
 165 170 175
 Ala Lys Asn Gln Lys Ile Tyr Leu Cys Gly Gly Asp Ala Lys Tyr Leu
 180 185 190
 Ser Ala Phe Leu Pro His Ser Val Cys Lys Glu Arg Leu Val Phe Asp
 195 200 205
 Gly Met Glu Ile Ala Leu Lys Lys Ala Gly Ile Leu Glu Cys Lys
 210 215 220

<210> 18
 <211> 267
 <212> PRT
 <213> Bordetella pertussis

<400> 18
 Met Ile Ile Leu Ile Asp Ser Gly Asn Ser Arg Leu Lys Val Gly Trp
 1 5 10 15
 Phe Asp Pro Asp Ala Pro Gln Ala Ala Arg Glu Pro Ala Pro Val Ala
 20 25 30
 Phe Asp Asn Leu Asp Leu Asp Ala Leu Gly Arg Trp Leu Ala Thr Leu
 35 40 45
 Pro Arg Arg Pro Gln Arg Ala Leu Gly Val Asn Val Ala Gly Leu Ala
 50 55 60
 Arg Gly Glu Ala Ile Ala Ala Thr Leu Arg Ala Gly Gly Cys Asp Ile
 65 70 75 80
 Arg Trp Leu Arg Ala Gln Pro Leu Ala Met Gly Leu Arg Asn Gly Tyr
 85 90 95
 Arg Asn Pro Asp Gln Leu Gly Ala Asp Arg Trp Ala Cys Met Val Gly
 100 105 110
 Val Leu Ala Arg Gln Pro Ser Val His Pro Pro Leu Leu Val Ala Ser
 115 120 125
 Phe Gly Thr Ala Thr Thr Leu Asp Thr Ile Gly Pro Asp Asn Val Phe
 130 135 140
 Pro Gly Gly Leu Ile Leu Pro Gly Pro Ala Met Met Arg Gly Ala Leu
 145 150 155 160
 Ala Tyr Gly Thr Ala His Leu Pro Leu Ala Asp Gly Leu Val Ala Asp
 165 170 175
 Tyr Pro Ile Asp Thr His Gln Ala Ile Ala Ser Gly Ile Ala Ala Ala
 180 185 190
 Gln Ala Gly Ala Ile Val Arg Gln Trp Leu Ala Gly Arg Gln Arg Tyr
 195 200 205

Gly Gln Ala Pro Glu Ile Tyr Val Ala Gly Gly Gly Trp Pro Glu Val
 210 215 220
 Arg Gln Glu Ala Glu Arg Leu Leu Ala Val Thr Gly Ala Ala Phe Gly
 225 230 235 240
 Ala Thr Pro Gln Pro Thr Tyr Leu Asp Ser Pro Val Leu Asp Gly Leu
 245 250 255
 Ala Ala Leu Ala Ala Gln Gly Ala Pro Thr Ala
 260 265

<210> 19
 <211> 777
 <212> DNA
 <213> Bacillus subtilis

<220>
 <221> CDS
 <222> (1)..(774)

<400> 19
 ttg tta ctg gtc atc gat gtg ggg aac acc aat act gta ctt ggt gta 48
 Leu Leu Leu Val Ile Asp Val Gly Asn Thr Asn Thr Val Leu Gly Val
 1 5 10 15
 tat cat gat gga aaa tta gaa tat cac tgg cgt ata gaa aca agc agg 96
 Tyr His Asp Gly Lys Leu Glu Tyr His Trp Arg Ile Glu Thr Ser Arg
 20 25 30
 cat aaa aca gaa gat gag ttt ggg atg att ttg cgt tcc tta ttt gat 144
 His Lys Thr Glu Asp Glu Phe Gly Met Ile Leu Arg Ser Leu Phe Asp
 35 40 45
 ctc tcc ggg ctt atg ttt gaa tag ata gat ggc att att att tcc tca 192
 His Ser Gly Leu Met Phe Glu Gln Ile Asp Gly Ile Ile Ile Ser Ser
 50 55 60
 gta gtg ccg cca atc atg ttt ggc tta gaa aga atg tcc aca aaa tac 240
 Val Val Pro Pro Ile Met Phe Ala Leu Glu Arg Met Cys Thr Lys Tyr
 65 70 75 80
 ttt cat atc gag cct caa att gtt ggt cca ggt atg aaa acc ggt tta 288
 Phe His Ile Glu Pro Gln Ile Val Gly Pro Gly Met Lys Thr Gly Leu
 85 90 95
 gat ata aaa tat gat aat ccg aca gaa gta ggg gta tac aca atc gta 336
 Asn Ile Lys Tyr Asp Asn Pro Lys Glu Val Gly Ala Asp Arg Ile Val
 100 105 110
 aat gtc gtc act gag ata cac ttg tac ggc aat cca tta att att atc 384
 Asn Ala Val Ala Ala Ile His Leu Tyr Gly Asn Pro Leu Ile Val Val
 115 120 125
 tat ttc aca att ggc aca atg tac ttc tac att tat tta att aca caa 432
 Asp Phe Gly Thr Ala Thr Thr Tyr Lys Tyr Ile Asp Glu Asn Lys Gln
 130 135 140
 tac atg ttc att att att att ggc att att att att att att att att 480
 Tyr Met Gly Gly Ala Ile Ala Ser Gly Ile Thr Ile Thr Thr Thr Thr
 145 150 155

145		150		155		160	
att tac tag agt gca gca aag att cct cgt atc gaa atc acc cgg ccc							625
Leu Tyr Ser Arg Ala Ala Lys Leu Pro Arg Ile Glu Ile Thr Arg Pro							
		165		170		175	
gac aat att atc gga aaa aac aac gtt agc gag atg cca tct gga att							576
Asp Asn Ile Ile Gly Lys Asn Thr Val Ser Ala Met Gln Ser Gly Ile							
		180		185		190	
tta ttt ggc tat gtc ggc caa gtg gaa gga atc gtt aag cga atg aaa							624
Leu Phe Gly Tyr Val Gly Gln Val Glu Gly Ile Val Lys Arg Met Lys							
		195		200		205	
agg tag gca aaa cag gac ctc aag gtc att gag aca gga ggc cag gag							672
Tyr Gln Ala Lys Gln Asp Leu Lys Val Ile Ala Thr Gly Gly Leu Ala							
		210		215		220	
cag atc att gag aac gaa tca gat tgt ata gac atc gtt gat cca ttc							720
Pro Leu Ile Ala Asn Glu Ser Asp Cys Ile Asp Ile Val Asp Pro Phe							
		225		230		235	240
tta acc cta aaa ggg ctg gaa ttg att tat gaa aga aac cgc gta gga							768
Leu Thr Leu Lys Gly Leu Glu Leu Ile Tyr Glu Arg Asn Arg Val Gly							
		245		250		255	
agt gta tag							777
Ser Val							

<210> 20
 <211> 960
 <212> DNA
 <213> Bacillus subtilis

<220>
 <221> CDS
 <222> (1)...(967)

<400> 20	
gtg aaa aat aaa gaa ctt aac cta cat act tta tac aca cag cac aat	48
Met Lys Asn Lys Glu Leu Asn Leu His Thr Leu Tyr Thr Gln His Asn	
1 8 10 18	
cgg gag tct tag tct agt ttt gag gag cat ttg tag att gat gta tct	96
Arg Glu Ser Trp Ser Gly Phe Gly Gly His Leu Ser Ile Ala Val Ser	
22 28 37	
gaa gaa gag gca aaa gct gtg aac gaa ctg aat gat tat cta tct att	144
Glu Glu Glu Ala Lys Ala Val Glu Gly Leu Asn Asp Tyr Leu Ser Val	
35 42 48	
gaa gaa ctg gag aag atc tat att cag ctc gtt cga ttc ctt cat tta	192
Gln Glu Val Glu Thr Ile Tyr Ile Pro Leu Val Arg Leu Leu His Leu	
52 61 67	
tat ttt aat tct ggt ggt tta ttt gat aat att gtc aat att ttt ttg	240
His Val Tyr Ser Ala Ala Glu Arg Asn Lys His Val Asn Val Phe Leu	
70 78 87	
aat tat cta cat tta ggt aac att ttt att att att att att att	288

Lys	His	Pro	His	Ser	Ala	Lys	Ile	Pro	Phe	Ile	Ile	Gly	Ile	Ala	Gly	
				85					90					95		
agt	gtc	gta	gtc	gga	aaa	agc	acg	acg	ggg	ggg	atc	ttg	cag	aag	ctg	336
Ser	Val	Ala	Val	Gly	Lys	Ser	Thr	Thr	Ala	Arg	Ile	Leu	Gln	Lys	Leu	
			100					105					110			
ctt	cag	agt	ttg	ccg	gac	agt	cga	aaa	gtg	agc	ctt	atc	acg	aca	gat	384
Leu	Ser	Arg	Leu	Pro	Asp	Arg	Pro	Lys	Val	Ser	Leu	Ile	Thr	Thr	Asp	
		115					120					125				
ggg	ttt	tta	ttt	ccg	act	gac	gag	ctg	aaa	aag	aaa	aat	atg	atg	tca	432
Gly	Phe	Leu	Phe	Pro	Thr	Ala	Glu	Leu	Lys	Lys	Lys	Asn	Met	Met	Ser	
	130					135					140					
aga	aaa	gga	ttt	ccg	gaa	agc	tat	gat	gta	aag	ggg	ctg	ctc	gaa	ttt	480
Arg	Lys	Gly	Phe	Pro	Glu	Ser	Tyr	Asp	Val	Lys	Ala	Leu	Leu	Glu	Phe	
	145				150					155					160	
ttg	aat	gac	tta	aaa	tca	gga	aag	gac	agc	gta	aag	ggc	ccg	gtg	tat	528
Leu	Asn	Asp	Leu	Lys	Ser	Gly	Lys	Asp	Ser	Val	Lys	Ala	Pro	Val	Tyr	
				165				170						175		
ccc	cat	cta	acc	tat	gac	cgc	gag	gaa	ggg	gtg	ttc	gag	gtt	gta	gaa	576
Ser	His	Leu	Thr	Tyr	Asp	Arg	Glu	Glu	Gly	Val	Phe	Glu	Val	Val	Glu	
			180					185					190			
cag	gag	gat	att	gtg	att	att	gaa	ggc	att	aat	gtt	ctt	cag	tgg	ccc	624
Gln	Ala	Asp	Ile	Val	Ile	Ile	Glu	Gly	Ile	Asn	Val	Leu	Gln	Ser	Pro	
		195					200					205				
acc	ttg	gag	gat	gac	cgg	gaa	aac	cag	cgt	att	ttt	gtt	ccg	gat	ttc	672
Thr	Leu	Glu	Asp	Asp	Arg	Glu	Asn	Pro	Arg	Ile	Phe	Val	Ser	Asp	Phe	
	210					215					220					
ttt	gat	ttt	cag	att	tat	gtg	gat	ggg	gag	gaa	agc	ggg	act	ttc	act	720
Phe	Asp	Phe	Ser	Ile	Tyr	Val	Asp	Ala	Glu	Glu	Ser	Arg	Ile	Phe	Thr	
	225				230				235						240	
ttg	tat	tta	gag	cgt	ttt	cgc	ctg	ctt	cgg	gaa	aca	gct	ttt	caa	aat	768
Trp	Tyr	Leu	Glu	Arg	Phe	Arg	Leu	Leu	Arg	Glu	Thr	Ala	Phe	Gln	Asn	
				245				250						255		
ccg	gat	tca	tat	ttt	cat	aaa	ttt	aaa	gac	ttg	ccc	gat	cag	gag	gat	816
Pro	Asp	Ser	Tyr	Phe	His	Lys	Phe	Lys	Asp	Leu	Ser	Asp	Gln	Glu	Ala	
			260				265						270			
gac	gag	atg	gca	ggc	tgg	att	tgg	ggg	agt	gtc	aac	tgg	cgg	aat	tta	864
Asp	Glu	Met	Ala	Ala	Ser	Ile	Trp	Glu	Ser	Val	Asn	Arg	Pro	Asn	Leu	
		275					280					285				
tat	gaa	aat	att	ttg	cga	act	aaa	ttc	agg	tca	gat	ctc	act	ttg	cgt	912
Tyr	Glu	Asn	Ile	Leu	Pro	Thr	Lys	Phe	Arg	Ser	Asp	Leu	Ile	Leu	Arg	
	290					295					300					
aaa	tta	gac	gtg	tat	aat	ttc	gat	tta	gtg	ttc	gtc	gtg	gtg	tta	tta	960
Lys	Gly	Asp	Gly	His	Lys	Val	Gln	Gln	Val	Leu	Val	Arg	Arg	Val		
	305				310						315					

101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525	526	527	528	529	530	531	532	533	534	535	536	537	538	539	540	541	542	543	544	545	546	547	548	549	550	551	552	553	554
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gaa agc cgg att ttc act tgg tat tta gag cgt ttt cgc ctg ctt cgg	672
Glu Ser Arg Ile Phe Thr Trp Tyr Leu Glu Arg Phe Arg Leu Leu Arg	
210 215 220	
gaa aca gcc ttt caa aat cct gat tca tat ttt cat aaa ttt aaa gac	720
Glu Thr Ala Phe Gln Asn Pro Asp Ser Tyr Phe His Lys Phe Lys Asp	
225 230 235 240	
ttg tcc gat cag gag gcc gac gag atg gca gcc tgg att tgg gag agt	768
Leu Ser Asp Gln Glu Ala Asp Glu Met Ala Ala Ser Ile Trp Glu Ser	
245 250 255 260	
gtc aac cgg cag aat tta tat gaa aat att ttg cca act aaa ttc agg	816
Val Asn Arg Pro Asn Leu Tyr Glu Asn Ile Leu Pro Thr Lys Phe Arg	
260 265 270	
tca gat ctc att ttg cgt aag gga gac ggg cat aag gtc gag gaa gtg	864
Ser Asp Leu Ile Leu Arg Lys Gly Asp Gly His Lys Val Glu Glu Val	
275 280 285	
ttg gta agg agg gta tga	882
Leu Val Arg Arg Val	
290	

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Met Glu Gly Leu Asn Asp Tyr Leu Ser Val Glu Glu Val Glu Thr Ile	
1 5 10 15	
tat att cgg ctt gtt cgc ttg ctt cat tta cat gtc aag tct aca gct	96
Tyr Ile Pro Leu Val Arg Leu Leu His Leu His Val Lys Ser Ala Ala	
20 25 30	
gaa cgc aat aag cat gtc aat gtt ttt ttg aag cac cca cat tca gac	144
Glu Arg Asn Lys His Val Asn Val Phe Leu Lys His Pro His Ser Ala	
35 40 45	
aaa att cgg ttt att aac ggc att gat ggt aat ttc aca atc gga aac	192
Lys Ile Pro Phe Ile Ile Gly Ile Ala Gly Ser Val Ala Val Gly Lys	
50 55 60	
agc acg acg agc agc atc ttg cag aag cta att ttg cgt ttg ctt gac	240
Ser Thr Thr Ala Arg Ile Leu Gln Lys Leu Leu Ser Arg Leu Pro Asp	
65 70 75	
ggt cca aaa ggt att att att aat aca gat ggt ttt tta ttt att att	288
Arg Pro Lys Val Ser Leu Ile Thr Thr Asp Gly Ile Leu Ile Pro Thr	
80 85 90 95	
ttt ttt ttt aat aat aat aat att att att att att att att att att	336
Ala Ala Leu Lys Lys Lys Asn Met Met Ser Asn Lys Gly Ile Pro Ile	

[illegible]

att	gtc	atg	ctg	acc	gct	tat	gat	tat	cag	gca	ggt	aaa	ctt	gct	gaa	96
ile	val	met	leu	thr	ala	tyr	asp	tyr	pro	ala	ala	lys	leu	ala	glu	
			20					25					30			
aaa	ggg	gga	gtt	gac	atg	att	tta	gtc	ggg	gat	tca	ctt	gga	atg	gtc	144
gin	ala	gly	val	asp	met	ile	leu	val	gly	asp	ser	leu	gly	met	val	
		36					40					45				
gtc	ctc	ggc	ctt	gat	tca	act	gtc	ggg	gtg	aca	ggt	ggg	gac	atg	atc	192
val	leu	gly	leu	asp	ser	thr	val	gly	val	thr	val	ala	asp	met	ile	
	51					55					60					
cat	cat	aca	aaa	gac	gtt	aaa	agg	ggt	ggg	ccg	aat	acc	ttt	att	gtg	240
his	his	thr	lys	ala	val	lys	arg	gly	ala	pro	asn	thr	phe	ile	val	
					70					75					80	
aca	gat	atg	ccg	ttt	atg	tct	tat	cac	ctg	tct	aag	gaa	gat	acg	ctg	288
thr	asp	met	pro	phe	met	ser	tyr	his	leu	ser	lys	glu	asp	thr	leu	
				85					90					95		
aaa	aat	gca	ggg	gct	atc	gtt	cag	gaa	agc	gga	gct	gac	gca	ctg	aag	336
lys	asn	ala	ala	ala	ile	val	gln	glu	ser	gly	ala	asp	ala	leu	lys	
			100					105					110			
ctt	gag	ggc	gga	gaa	ggc	gtg	ttt	gaa	tcc	att	ggc	gca	ttg	acg	att	384
leu	glu	gly	gly	glu	gly	val	phe	glu	ser	ile	arg	ala	leu	thr	leu	
		115					120					125				
gga	ggc	att	cca	gta	gtc	agt	cac	tta	ggg	ttg	aca	ctg	cag	tca	gtc	432
gly	gly	ile	pro	val	val	ser	his	leu	gly	leu	thr	pro	gln	ser	val	
		130				135					140					
ggg	gtt	ctg	ggc	ggc	tat	aaa	gta	cag	ggc	aaa	gac	gta	cac	att	gtc	480
gly	val	leu	gly	gly	tyr	lys	val	gln	gly	lys	asp	gln	gln	ser	ala	
			145		150					155					160	
aaa	aaa	tta	ata	gaa	gac	agt	ata	aaa	tgc	gaa	gaa	gca	gga	ggt	atg	528
lys	lys	leu	ile	gln	asp	ser	ile	lys	cys	gln	gln	ala	gly	ala	met	
				165					170					175		
atg	ctt	gtg	ctg	aaa	tgt	gtg	ccg	aca	gaa	ctc	cca	ggt	aaa	att	gac	576
met	leu	val	leu	ala	cys	val	pro	ala	glu	leu	thr	ala	lys	ile	ala	
			180					185					190			
gag	acn	cta	agg	ata	ccg	gtc	att	gga	atc	ggg	gct	ggt	gtg	aaa	acg	624
glu	thr	leu	ser	ile	pro	val	ile	gly	ile	gly	ala	gly	val	lys	ala	
		195					200					205				
gac	gga	cac	gtt	ctc	gtt	tat	cat	tat	att	atc	ggc	cac	ggt	gtt	gag	672
asp	gly	gln	val	leu	val	tyr	his	asp	ile	ile	gly	his	gly	val	gln	
						210					220					
tta	ata	tct	aaa	ttt	gta	aaa	cac	tat	agg	ttt	att	tat	aaa			

Pro Glu Gln Lys His Ser Phe Gln Met Asn Gln Thr Val Leu Asp Gly
 260 265 270

tgg tac ggg gga aaa
 Leu Tyr Gly Gly Lys
 275

831

<210> 24
 <211> 277
 <212> PRT
 <213> Bacillus subtilis

<400> 24
 Met Lys Thr Lys Leu Asp Phe Leu Lys Met Lys Glu Ser Glu Glu Pro
 1 5 10 15
 Ile Val Met Leu Thr Ala Tyr Asp Tyr Pro Ala Ala Lys Leu Ala Glu
 20 25 30
 Gln Ala Gly Val Asp Met Ile Leu Val Gly Asp Ser Leu Gly Met Val
 35 40 45
 Val Leu Gly Leu Asp Ser Thr Val Gly Val Thr Val Ala Asp Met Ile
 50 55 60
 His His Thr Lys Ala Val Lys Arg Gly Ala Pro Asn Thr Phe Ile Val
 65 70 75 80
 Thr Asp Met Pro Phe Met Ser Tyr His Leu Ser Lys Glu Asp Thr Leu
 85 90 95
 Lys Asn Ala Ala Ala Ile Val Gln Glu Ser Gly Ala Asp Ala Leu Lys
 100 105 110
 Leu Glu Gly Gly Glu Gly Val Phe Glu Ser Ile Arg Ala Leu Thr Leu
 115 120 125
 Gly Gly Ile Pro Val Val Ser His Leu Gly Leu Thr Pro Gln Ser Val
 130 135 140
 Gly Val Leu Gly Gly Tyr Lys Val Gln Gly Lys Asp Glu Gln Ser Ala
 145 150 155 160
 Lys Lys Leu Ile Glu Asp Ser Ile Lys Cys Glu Glu Ala Gly Ala Met
 165 170 175
 Met Leu Val Leu Glu Lys Val Pro Ala Glu Leu Thr Ala Lys Ile Ala
 180 185 190
 Glu Thr Leu Ser Ile Pro Val Ile Gly Ile Gly Ala Gly Val Lys Ala
 195 200 205
 Asp Gly Gln Val Leu Val Tyr His Asp Ile Ile Gly His Gly Val Gln
 210 215 220
 Arg Thr Arg Lys Phe Val Lys Gln Tyr Thr Arg Ile Asp Glu Thr Ile
 225 230 235 240
 Gln Thr Ala Ile Ser Gly Tyr Val Gln Asp Val Arg His Arg Ala Ile
 245 250 255

Pro Glu Gln Lys His Ser Phe Gln Met Asn Gln Thr Val Leu Asp Gly
 260 265 270

Leu Tyr Gly Gly Lys
 275

<210> 25

<211> 658

<212> DNA

<213> Bacillus subtilis

<220>

<221> CDS

<222> (1)..(858)

<400> 25

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 Met Arg Gln Ile Thr Asp Ile Ser Gln Leu Lys Glu Ala Ile Lys Gln
 1 5 10 15

tac cat tca gag gcc aag tca atc gga ttt gtt cag acg atg ggg ttt 96
 Tyr His Ser Glu Gly Lys Ser Ile Gly Phe Val Pro Thr Met Gly Phe
 20 25 30

atg cat gag ggg cat tta acc tta gca gac aaa gca aga caa gaa aac 144
 Leu His Glu Gly His Leu Thr Leu Ala Asp Lys Ala Arg Gln Glu Asn
 35 40 45

gac gcc gtc att atg agt att ttt gtg aat cct gca caa ttc ggc cct 192
 Asp Ala Val Ile Met Ser Ile Phe Val Asn Pro Ala Gln Phe Gly Pro
 50 55 60

aat gaa gat ttt gaa gca tat cag cgc gat att gag cgg gat tta gct 240
 Asn Glu Asp Phe Glu Ala Tyr Pro Arg Asp Ile Glu Arg Asp Ala Ala
 65 70 75 80

ctt gca gaa aac gcc gga gtc gat att ctt ttt acg cca gat gct cat 288
 Leu Ala Glu Asn Ala Gly Val Asp Ile Leu Phe Thr Pro Asp Ala His
 85 90 95

gat atg tat ccc ggt gaa aag aat gtc acg att cat gta gaa aga cgc 336
 Asp Met Tyr Pro Gly Glu Lys Asn Val Thr Ile His Val Glu Arg Arg
 100 105 110

aca aac gta tta tgc ggg cag tca aga gaa gaa cat ttt att tta gtc 384
 Thr Asp Val Leu Cys Gly Arg Ser Arg Gln Gly His Phe Asp Gly Val
 115 120 125

gaa atc gta tta acg aag ctt ttc aat cta gtc aag cag att agt gcc 432
 Ala Ile Val Leu Thr Lys Leu Phe Asn Leu Val Lys Pro Thr Arg Ala
 130 135 140

tat tta att tta aaa gat cag tat tat tat tta att gtt att tta tta 480
 Tyr Phe Gly Leu Lys Asp Ala Gln Gln Val Ala Val Val Asp Gly Leu
 145 150 155 160

atc att gta tta ttc aag tat att gaa tta att att gaa att att gaa 528
 Ile Ser Asp Phe Phe Met Asp Ile Gln Leu Val Pro Val Arg Thr Val
 165 170 175 180

aga gag gaa gac ggc tta gcc aaa agc tct cgc aat gta tac tta aca 576
 Arg Glu Glu Asp Gly Leu Ala Lys Ser Ser Arg Asn Val Tyr Leu Thr
 187 188 190

gct gag gaa aga aaa gaa gcg cct aag ctg tat cgg gcc ctt caa aca 624
 Ala Glu Glu Arg Lys Glu Ala Pro Lys Leu Tyr Arg Ala Leu Gln Thr
 195 200 205

agt gcg gaa ctt gtc caa gcc ggt gaa aga gat cct gaa gcg ctg ata 672
 Ser Ala Glu Leu Val Gln Ala Gly Glu Arg Asp Pro Glu Ala Val Ile
 210 215 220

aaa gct gca aaa gat atc att gaa acg act agc gga acc ata gac tat 720
 Lys Ala Ala Lys Asp Ile Ile Glu Thr Thr Ser Gly Thr Ile Asp Tyr
 225 230 235 240

gta gag ctt tat tcc tat ccg gaa ttc gag cct ctg aat gaa att gct 768
 Val Glu Leu Tyr Ser Tyr Pro Glu Leu Glu Pro Val Asn Glu Ile Ala
 245 250 255

gga aag atg att ctc gct gtt gca gtt gct ttt tca aaa gcg cgt tta 816
 Gly Lys Met Ile Leu Ala Val Ala Val Ala Phe Ser Lys Ala Arg Leu
 260 265 270

ata gat aat atc att att gat att cga gaa atg gag aga ata 868
 Ile Asp Asn Ile Ile Ile Asp Ile Arg Glu Met Glu Arg Ile
 275 280 285

<210> 26
 <211> 286
 <212> 887
 <213> *Bacillus subtilis*

<400> 16
 Met Arg Gln Ile Thr Asp Ile Ser Gln Leu Lys Glu Ala Ile Lys Gln
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Tyr His Ser Glu Gly Lys Ser Ile Gly Phe Val Pro Thr Met Gly Phe
 20 25 30

Leu His Glu Gly His Leu Thr Leu Ala Asp Lys Ala Arg Gln Glu Asn
 35 40 45

Asp Ala Val Ile Met Ser Ile Phe Val Asn Pro Ala Gln Phe Gly Pro
 50 55 60

Asn Glu Asp Phe Glu Ala Tyr Pro Arg Asp Ile Glu Arg Asp Ala Ala
 65 70 75 80

Leu Ala Glu Asn Ala Gly Val Asp Ile Leu Phe Thr Pro Asp Ala His
 85 90 95

Asp Met Tyr Pro Gly Glu Lys Asn Val Thr Ile His Val Glu Arg Arg
 100 105 110 115

Thr Asp Val Leu Tyr Gly Arg Ser Arg Glu Gly His Phe Asp Gly Val
 120 125 130

Ala Ile Val Leu Thr Lys Leu Phe Asn Leu Val Lys Pro Thr Arg Ala
 135 140 145 150

130	135	140
Tyr Phe Gly Leu Lys Asp Ala Gln Gln Val Ala Val Val Asp Gly Leu 145 150 155 160		
Ile Ser Asp Phe Phe Met Asp Ile Glu Leu Val Pro Val Asp Thr Val 165 170 175		
Arg Glu Glu Asp Gly Leu Ala Lys Ser Ser Arg Asn Val Tyr Leu Thr 181 185 190		
Ala Glu Glu Arg Lys Glu Ala Pro Lys Leu Tyr Arg Ala Leu Gln Thr 195 200 205		
Ser Ala Glu Leu Val Gln Ala Gly Glu Arg Asp Pro Glu Ala Val Ile 210 215 220		
Lys Ala Ala Lys Asp Ile Ile Glu Thr Thr Ser Gly Thr Ile Asp Tyr 225 230 235 240		
Val Glu Leu Tyr Ser Tyr Pro Glu Leu Glu Pro Val Asn Glu Ile Ala 245 250 255		
Gly Lys Met Ile Leu Ala Val Ala Val Ala Phe Ser Lys Ala Arg Leu 260 265 270		
Ile Asp Asn Ile Ile Ile Asp Ile Arg Glu Met Glu Arg Ile 275 280 285		

<210> 27
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<220>
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gaa gaa aac ctg aac tat gtg gga agc att aca att gat gaa gat ctg Glu Ala Asn Leu Asn Tyr Val Gly Ser Ile Thr Ile Asp Glu Asp Leu 20 25 30 36	
att gat acg atg gga atg att cct aat gaa aaa gta gaa att gtg aat Ile Asp Ala Val Gly Met Leu Pro Asn Glu Lys Val Gln Ile Val Asn 35 40 46	144
aat aat aat gaa gaa cgt att gaa acg tac att att ctt ggt gaa cgt Asn Asn Asn Gly Ala Arg Leu Gln Thr Tyr Ile Ile Pro Gly Lys Arg 45 50 55 60 66	149
aga att att gta gta tat tta att att tta att gaa att att att att Gly Ser Gly Val Ile Tyr Leu Asn Gly Ala Ala Ala Arg Leu Val Gln 65 70 75 80 86	149
taa tta att att att att att att att att att att att att att att 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255	187

Glu Gly Asp Lys Val Ile Ile Ile Ser Tyr Lys Met Met Ser Asp Gln
 85 90 95

gaa gag gaa agc cat gag cag aaa gtg ggt gtt ctg aat gat caa aac 336
 Glu Ala Ala Ser His Glu Pro Lys Val Ala Val Leu Asn Asp Gln Asn
 100 105 110

aaa att gaa caa atg ctg ggg aac gaa caa gcc cgt aca att tlg 331
 Lys Ile Glu Gln Met Leu Gly Asn Glu Pro Ala Arg Thr Ile Leu
 115 120 125

<210> 28
 <211> 127
 <212> PRT
 <213> Bacillus subtilis

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 1 5 10 15

Glu Ala Asn Leu Asn Tyr Val Gly Ser Ile Thr Ile Asp Glu Asp Leu
 20 25 30

Ile Asp Ala Val Gly Met Leu Pro Asn Glu Lys Val Gln Ile Val Asn
 35 40 45

Asn Asn Asn Gly Ala Arg Leu Glu Thr Tyr Ile Ile Pro Gly Lys Arg
 50 55 60

Gly Ser Gly Val Ile Cys Leu Asn Gly Ala Ala Ala Arg Leu Val Gln
 65 70 75 80

Glu Gly Asp Lys Val Ile Ile Ile Ser Tyr Lys Met Met Ser Asp Gln
 85 90 95

Glu Ala Ala Ser His Glu Pro Lys Val Ala Val Leu Asn Asp Gln Asn
 100 105 110

Lys Ile Glu Gln Met Leu Gly Asn Glu Pro Ala Arg Thr Ile Leu
 115 120 125

<210> 28
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 <212> DNA
 <213> Bacillus subtilis

<220>
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 <222> (1)...(894)

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 Met Lys Ile Gly Ile Ile Gly Gly Gly Ser Val Gly Leu Leu Lys Ala
 1 5 10 15

tat tat ttt ttt att tat tat ttt ttt ttt ttt ttt ttt ttt ttt ttt 49
 Tyr Tyr Leu Ser Leu Tyr His Asp Val Thr Val Val Thr Arg Arg Gln
 20 25 30 35 40

gaa	cag	gct	gag	gac	att	cag	tct	gaa	gga	atc	cgg	ctt	tat	aaa	ggc	144
Glu	Gln	Ala	Ala	Ala	Ile	Gln	Ser	Glu	Gly	Ile	Arg	Leu	Tyr	Lys	Gly	
		35					40					45				
ggg	gag	gaa	ttc	agg	gct	gat	tgc	agt	gag	gac	acg	agt	atc	aat	tcc	142
Gly	Glu	Glu	Phe	Arg	Ala	Asp	Cys	Ser	Ala	Asp	Thr	Ser	Ile	Asn	Ser	
		50					55				60					
gac	ttt	gac	ctg	ctt	gtc	gtg	aca	gtg	aag	cag	cat	cag	ctt	aaa	tct	240
Asp	Phe	Asp	Leu	Leu	Val	Val	Thr	Val	Lys	Gln	His	Gln	Leu	Gln	Ser	
		65			70					75					80	
gtt	ttt	tcc	tcc	ctt	gaa	cga	atc	ggg	aag	acg	aat	ata	tta	ttt	ttg	238
Val	Phe	Ser	Ser	Leu	Glu	Arg	Ile	Gly	Lys	Thr	Asn	Ile	Leu	Phe	Leu	
				85					90					95		
caa	aac	ggc	atg	ggg	cat	atc	caac	gac	cta	aaa	gac	tgg	caa	glt	ggc	336
Gln	Asn	Gly	Met	Gly	His	Ile	His	Asp	Leu	Lys	Asp	Trp	His	Val	Gly	
			100					105					110			
cat	tcc	att	tat	gtt	gga	atc	gtt	gag	caac	gga	gct	gta	aga	aaa	tcc	384
His	Ser	Ile	Tyr	Val	Gly	Ile	Val	Glu	His	Gly	Ala	Val	Arg	Lys	Ser	
		115					120					125				
gat	aca	gct	gtt	gat	cat	aca	ggc	cta	ggt	gcg	ata	aaa	tgg	agc	ggc	432
Asp	Thr	Ala	Val	Asp	His	Thr	Gly	Leu	Gly	Ala	Ile	Lys	Trp	Ser	Ala	
		130					135				140					
ttc	gac	gat	gct	gaa	caa	gac	cgg	ctg	aac	atc	ttg	ttt	cag	cat	aac	480
Phe	Asp	Asp	Ala	Glu	Pro	Asp	Arg	Leu	Asn	Ile	Leu	Phe	Gln	His	Asn	
					150					155					160	
cat	tcc	gat	ttt	cgc	att	tat	tat	cag	arg	gat	tgg	tac	cgt	cta	crg	528
His	Ser	Asp	Phe	Pro	Ile	Tyr	Tyr	Glu	Thr	Asp	Trp	Tyr	Arg	Leu	Leu	
				165				170					175			
aca	ggc	aag	ctg	att	gta	aat	ggc	tgt	att	aat	cct	tta	aat	ggc	tta	576
Thr	Gly	Lys	Leu	Ile	Val	Asn	Ala	Cys	Ile	Asn	Pro	Leu	Thr	Ala	Leu	
			180					185				190				
ttg	caa	gtg	aaa	aat	gga	gaa	ctg	cta	aca	acg	caa	gct	tat	ctg	gct	624
Leu	Gln	Val	Lys	Asn	Gly	Glu	Leu	Leu	Thr	Thr	Pro	Ala	Tyr	Leu	Ala	
		195					200					205				
ttt	atg	aag	ctg	gta	ttt	cag	cag	gca	tgt	cgc	att	tta	aaa	ctt	gaa	672
Phe	Met	Lys	Leu	Val	Phe	Gln	Glu	Ala	Cys	Arg	Ile	Leu	Lys	Leu	Glu	
	210					215					220					
aat	gaa	gaa	aag	gct	tgg	gag	cgg	gtt	caa	gct	gtt	tgt	ggc	caa	acg	720
Asn	Glu	Glu	Lys	Ala	Trp	Glu	Arg	Val	Gln	Ala	Val	Cys	Gly	Gln	Thr	
					230					235					240	
aaa	gag	aat	ctt	tca	tca	atc	ctc	gtt	gac	gtc	ata	ggt				

Gln Gly Leu Asp Ala Val His Leu Glu Phe Leu Tyr Gly Ser Ile Lys
 275 285 285

gca ttg gag cga aat aca aac aaa gtc ttt
 Ala Leu Glu Arg Asn Thr Asn Lys Val Phe
 290 295

894

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Tyr Tyr Leu Ser Leu Tyr His Asp Val Thr Val Val Thr Arg Arg Gln
 20 25 30

Glu Gln Ala Ala Ala Ile Gln Ser Glu Gly Ile Arg Leu Tyr Lys Gly
 35 40 45

Gly Glu Glu Phe Arg Ala Asp Cys Ser Ala Asp Thr Ser Ile Asn Ser
 50 55 60

Asp Phe Asp Leu Leu Val Val Thr Val Lys Gln His Gln Leu Gln Ser
 65 70 75 80

Val Phe Ser Ser Leu Glu Arg Ile Gly Lys Thr Asn Ile Leu Phe Leu
 85 90 95

Gln Asn Gly Met Gly His Ile His Asp Leu Lys Asp Trp His Val Gly
 100 105 110

His Ser Ile Tyr Val Gly Ile Val Glu His Gly Ala Val Arg Lys Ser
 115 120 125

Asp Thr Ala Val Asp His Thr Gly Leu Gly Ala Ile Lys Trp Ser Ala
 130 135 140

Phe Asp Asp Ala Glu Pro Asp Arg Leu Asn Ile Leu Phe Gln His Asn
 145 150 155 160

His Ser Asp Phe Pro Ile Tyr Tyr Gln Thr Asp Trp Tyr Arg Leu Leu
 165 170 175

Thr Gly Lys Leu Ile Val Asn Ala Cys Ile Asn Pro Leu Thr Ala Leu
 180 185 190

Leu Gln Val Lys Asn Gly Glu Leu Leu Thr Thr Pro Ala Tyr Leu Ala
 195 200 205

Phe Met Lys Leu Val Phe Gln Gln Ala Cys Arg Ile Leu Lys Leu Gln
 210 215 220

Asn Gln Gln Lys Ala Trp Gln Arg Val Gln Ala Val Cys Gly Gln Thr
 225 230 235 240

Lys Gln Asn Arg Ser Ser Met Leu Val Asp Val Ile Gly Gly Arg Gln
 245 250 255

Thr Glu Ala Asp Ala Ile Ile Gly Tyr Leu Leu Lys Glu Ala Ser Leu
 280 285 290

Gln Gly Leu Asp Ala Val His Leu Glu Phe Leu Tyr Gly Ser Ile Lys
 275 280 285

Ala Leu Glu Arg Asn Thr Asn Lys Val Phe
 290 295

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 Met Gly Thr Asn Val Gln Val Asp Ser Ala Ser Ala Glu Cys Thr Gln
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acg atg agc gga gca tta atg atg att gaa tca tta aaa aaa gag aaa 96
 Thr Met Ser Gly Ala Leu Met Leu Ile Gln Ser Leu Lys Lys Glu Lys
 20 25 30

gta gaa atg atc ttc ggt tat ccg ggc ggg gct gtg att cca att tac 144
 Val Glu Met Ile Phe Gly Tyr Pro Gly Gly Ala Val Leu Pro Ile Tyr
 35 40 45

gat aag cta ttc aat tca ggg ttg gta cat atc att ccg ggt cca gaa 192
 Asp Lys Leu Tyr Asn Ser Gly Leu Val His Ile Leu Pro Arg His Glu
 50 55 60

caa gga gca att cat gca gcg gag gga tac gca agg gtc tcc gga aaa 240
 Gln Gly Ala Ile His Ala Ala Glu Gly Tyr Ala Arg Val Ser Gly Lys
 65 70 75 80

cca ggt gtc gtc att gcc acg tca ggg ccg gaa gac aca aac att gtt 288
 Pro Gly Val Val Ile Ala Thr Ser Gly Pro Gly Ala Thr Asn Leu Val
 85 90 95

aca ggc att gat gat gcc atg att att tca ttg ccg tta gtc ttc ttt 336
 Thr Gly Leu Ala Asp Ala Met Ile Asp Ser Leu Pro Leu Val Val Phe
 100 105 110 115

aca ggg cag gta gca acc tct gta atc ggg agc gat gca ttt cag aaa 384
 Thr Gly Gln Val Ala Thr Ser Val Ile Gly Ser Asp Ala Phe Glu Glu
 115 120 125 130

aca gat att tta ggt att acg atg tca tta aca aca ccc agc ttc cag 432
 Ala Asp Ile Leu Gly Ile Thr Met Pro Val Thr Lys His Ser Tyr Glu
 135 140 145

att ccc tta tta gaa tat ctc ccc ctc att att aca tta ggc ttc cat 480
 Val Arg Glu Ile Ala Asp Leu Ile Arg Ile Ile Lys Glu Ala Phe His
 145 150 155 160

att gca aca act gga aga ccc gga cct gta ttg att gat att cag aaa	828
Ile Ala Thr Thr Gly Arg Pro Gly Pro Val Leu Ile Asp Ile Pro Lys	
165 170 175	
gat gta gca aca att gaa gga gaa ttc agc tac gat cat gag atg aat	876
Asp Val Ala Thr Ile Glu Gly Glu Phe Ser Tyr Asp His Glu Met Asn	
185 190 195	
ctc cag gga tac cag cag aca aca gag cag aat tat ttg cag atc cgc	624
Leu Pro Gly Tyr Gln Pro Thr Thr Glu Pro Asn Tyr Leu Gln Ile Arg	
195 200 205	
aag ctt gtg gaa gcc gtg agc agt gag aaa aaa cag gtg atc ctg gag	672
Lys Leu Val Glu Ala Val Ser Ser Ala Lys Lys Pro Val Ile Leu Ala	
210 215 220	
ggc ggc ggc gta ctg cac gga aaa ggc tca gaa gaa tta aaa aat tat	720
Gly Ala Gly Val Leu His Gly Lys Ala Ser Glu Glu Leu Lys Asn Tyr	
225 230 235 240	
gct gaa cag cag caa atc cct gtg gca cac acc ctt ttg ggg ctc gga	768
Ala Glu Gln Gln Gln Ile Pro Val Ala His Thr Leu Leu Gly Leu Gly	
245 250 255	
ggc ttc cag gct gac cat cag ctt ttc cta ggc atg gag gga atg cac	816
Gly Phe Pro Ala Asp His Pro Leu Phe Leu Gly Met Ala Gly Met His	
260 265 270	
ggc act tat aca gcc aat atg gcc ctt cat gaa tgt gat cta tta atc	864
Gly Thr Tyr Thr Ala Asn Met Ala Leu His Glu Cys Asp Leu Leu Ile	
275 280 285	
agt atc gac gac cgt ttt gat gac ctt gta aca gga aac ctg aaa cac	912
Ser Ile Gly Ala Arg Phe Asp Asp Arg Val Thr Gly Asn Leu Lys His	
290 295 300	
ttt gcc aga aac gcc aag ata gcc cac atc gat att gat cca gct gaa	960
Phe Ala Arg Asn Ala Lys Ile Ala His Ile Asp Ile Asp Pro Ala Glu	
305 310 315 320	
att gga aaa atc atg aaa aca caa att cct gta gtc gga gac agc aaa	1008
Ile Gly Lys Ile Met Lys Thr Gln Ile Pro Val Val Gly Asp Ser Lys	
325 330 335	
att gtc ctg cag gaa ctg atc aaa caa gac gac aaa caa agc cat tca	1056
Ile Val Leu Gln Gln Leu Ile Lys Gln Asp Gly Lys Gln Ser Asp Ser	
340 345 350	
agc gaa tag aaa aaa caa ctc gta gaa tag aaa gaa gag tat cag ctc	1104
Ser Glu Trp Lys Lys Gln Leu Ala Glu Trp Lys Glu Glu Tyr Pro Leu	
355 360 365	
tag tat gta gat aat gaa gaa gaa ggt ctt aaa cct tag aaa ttt att	1152
Trp Tyr Val Asp Asn Glu Glu Glu Gly Phe Lys Pro Gln Lys Leu Ile	
365 370 375	
aaa tat att tat aaa ttt aca aaa gaa gaa gaa gaa gaa gaa gaa gaa	1200
Ala Tyr Ile His Gln Phe Thr Lys Gly Ala Ala Ile Val Ala Thr Asp	
375 380 385	
aaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa gaa	1248
Ala Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu	
385 390 395	

Val	Gly	Gln	His	Gln	Met	Trp	Ser	Ala	Gln	Phe	Tyr	Pro	Phe	Gln	Lys	
				405					410					415		
gca	gat	aaa	tgg	gtc	acg	tca	ggc	gga	ctt	gga	acg	atg	gga	ttc	ggc	1296
Ala	Asp	Lys	Trp	Val	Thr	Ser	Gly	Gly	Leu	Gly	Thr	Met	Gly	Phe	Gly	
			420					425					430			
ctt	ccg	ggg	ggg	atc	ggc	gca	cag	ctg	gac	gaa	aaa	gat	gct	act	gtt	1344
Leu	Pro	Ala	Ala	Ile	Gly	Ala	Gln	Leu	Ala	Glu	Lys	Asp	Ala	Thr	Val	
			435				440					445				
gtc	ggg	gtt	gtc	gga	gac	ggc	gga	ttc	caa	atg	acg	ctt	caa	gaa	ctc	1392
Val	Ala	Val	Val	Gly	Asp	Gly	Gly	Phe	Gln	Met	Thr	Leu	Gln	Glu	Leu	
	450					455					460					
gat	gtt	att	ggc	gaa	tta	aat	ctt	ccg	gtc	aag	gta	gtg	att	tta	aat	1440
Asp	Val	Ile	Arg	Glu	Leu	Asn	Leu	Pro	Val	Lys	Val	Val	Ile	Leu	Asn	
465					470					475					480	
aac	gct	tgt	ctc	gga	atg	gtc	aga	cag	tgg	cag	gaa	att	ttc	tat	gaa	1488
Asn	Ala	Cys	Leu	Gly	Met	Val	Arg	Gln	Trp	Gln	Glu	Ile	Phe	Tyr	Glu	
				485					490					495		
gaa	cgt	tat	tca	gaa	tct	aaa	ttc	gct	tct	cag	ccg	gac	ttc	gtc	aaa	1536
Glu	Arg	Tyr	Ser	Glu	Ser	Lys	Phe	Ala	Ser	Gln	Pro	Asp	Phe	Val	Lys	
			500					505					510			
ttg	tcc	gaa	gca	tac	ggc	att	aaa	ggc	atc	aga	att	tca	tca	gaa	ggc	1584
Leu	Ser	Glu	Ala	Tyr	Gly	Ile	Lys	Gly	Ile	Arg	Ile	Ser	Ser	Glu	Ala	
		515					520					525				
gaa	gca	aag	gaa	aag	ctg	gaa	gag	gaa	tta	aca	tca	aga	gaa	cct	gtt	1632
Glu	Ala	Lys	Glu	Lys	Leu	Gln	Gln	Ala	Leu	Thr	Ser	Arg	Gln	Pro	Val	
	530					535					540					
gtc	att	gac	gtg	ggg	gtt	gca	agc	gaa	gaa	aaa	gta	ttc	ccg	atg	gtg	1680
Val	Ile	Asp	Val	Arg	Val	Ala	Ser	Glu	Glu	Lys	Val	Phe	Pro	Met	Val	
545					550					555					560	
gct	ccg	ggg	aaa	ggg	ctg	cat	gaa	atg	gtg	ggg	gtg	aaa	ccg	tga		1728
Ala	Pro	Gly	Lys	Gly	Leu	His	Glu	Met	Val	Gly	Val	Lys	Pro			
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<211> 574

<212> ERI

<213> Bacillus subtilis

<400> 32

Met Gly Thr Asn Val Gln Val Asp Ser Ala Ser Ala Gln Lys Thr Gln
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Thr Met Ser Gly Ala Leu Met Leu Ile Gln Ser Leu Lys Lys Gln Lys
20 24 28 32

Val Gln Met Ile Ile Gly Tyr Pr Gly Gly Ala Val Leu Pro Ile Tyr
36 40 44 48

Asp Lys Leu Tyr Asn Ser Gly Leu Val His Ile Leu Pr Arg His Ala
52 56 60 64

Gln	Gly	Ala	Ile	His	Ala	Ala	Glu	Gly	Tyr	Ala	Arg	Val	Ser	Gly	Lys	65	70	75	80
Pro	Gly	Val	Val	Ile	Ala	Thr	Ser	Gly	Pro	Gly	Ala	Thr	Asn	Leu	Val	85	90	95	
Thr	Gly	Leu	Ala	Asp	Ala	Met	Ile	Asp	Ser	Leu	Pro	Leu	Val	Val	Phe	100	105	110	
Thr	Gly	Gln	Val	Ala	Thr	Ser	Val	Ile	Gly	Ser	Asp	Ala	Phe	Gln	Glu	115	120	125	
Ala	Asp	Ile	Leu	Gly	Ile	Thr	Met	Pro	Val	Thr	Lys	His	Ser	Tyr	Gln	130	135	140	
Val	Arg	Gln	Pro	Glu	Asp	Leu	Pro	Arg	Ile	Ile	Lys	Glu	Ala	Phe	His	145	150	155	160
Ile	Ala	Thr	Thr	Gly	Arg	Pro	Gly	Pro	Val	Leu	Ile	Asp	Ile	Pro	Lys	165	170	175	
Asp	Val	Ala	Thr	Ile	Glu	Gly	Glu	Phe	Ser	Tyr	Asp	His	Glu	Met	Asn	180	185	190	
Leu	Pro	Gly	Tyr	Gln	Pro	Thr	Thr	Glu	Pro	Asn	Tyr	Leu	Gln	Ile	Arg	195	200	205	
Lys	Leu	Val	Glu	Ala	Val	Ser	Ser	Ala	Lys	Lys	Pro	Val	Ile	Leu	Ala	210	215	220	
Gly	Ala	Gly	Val	Leu	His	Gly	Lys	Ala	Ser	Glu	Glu	Leu	Lys	Asn	Tyr	225	230	235	240
Ala	Glu	Gln	Gln	Gln	Ile	Pro	Val	Ala	His	Thr	Leu	Leu	Gly	Leu	Gly	245	250	255	
Gly	Phe	Pro	Ala	Asp	His	Pro	Leu	Phe	Leu	Gly	Met	Ala	Gly	Met	His	260	265	270	
Gly	Thr	Tyr	Thr	Ala	Asn	Met	Ala	Leu	His	Glu	Cys	Asp	Leu	Leu	Ile	275	280	285	
Ser	Ile	Gly	Ala	Arg	Phe	Asp	Asp	Arg	Val	Thr	Gly	Asn	Leu	Lys	His	290	295	300	
Phe	Ala	Arg	Asn	Ala	Lys	Ile	Ala	His	Ile	Asp	Ile	Asp	Pro	Ala	Glu	305	310	315	320
Ile	Gly	Lys	Ile	Met	Lys	Thr	Gln	Ile	Pro	Val	Val	Gly	Asp	Ser	Lys	325	330	335	
Ile	Val	Leu	Gln	Glu	Leu	Ile	Lys	Gln	Asp	Gly	Lys	Gln	Ser	Asp	Ser	340	345	350	
Ser	Gln	Tyr	Lys	Lys	Gln	Leu	Ala	Gln	Tyr	Lys	Gln	Gln	Tyr	Pro	Leu	355	360	365	
Tyr	Tyr	Val	Asp	Asn	Ala	His	Glu	Gly	Phe	Lys	Pro	Gln	Lys	Leu	Ile	370	375	380	

Ala Tyr Ile His Gln Phe Thr Lys Gly Glu Ala Ile Val Ala Thr Asp
 385 390 395 400
 Val Gly Gln His Gln Met Trp Ser Ala Gln Phe Tyr Pro Phe Gln Lys
 405 410 415
 Ala Asp Lys Trp Val Thr Ser Gly Gly Leu Gly Thr Met Gly Phe Gly
 420 425 430
 Leu Pro Ala Ala Ile Gly Ala Gln Leu Ala Glu Lys Asp Ala Thr Val
 435 440 445
 Val Ala Val Val Gly Asp Gly Gly Phe Gln Met Thr Leu Gln Glu Leu
 450 455 460
 Asp Val Ile Arg Glu Leu Asn Leu Pro Val Lys Val Val Ile Leu Asn
 465 470 475 480
 Asn Ala Cys Leu Gly Met Val Arg Gln Trp Gln Glu Ile Phe Tyr Glu
 485 490 495
 Glu Arg Tyr Ser Glu Ser Lys Phe Ala Ser Gln Pro Asp Phe Val Lys
 500 505 510
 Leu Ser Glu Ala Tyr Gly Ile Lys Gly Ile Arg Ile Ser Ser Glu Ala
 515 520 525
 Glu Ala Lys Glu Lys Leu Glu Glu Ala Leu Thr Ser Arg Glu Pro Val
 530 535 540
 Val Ile Asp Val Arg Val Ala Ser Glu Glu Lys Val Phe Pro Met Val
 545 550 555 560
 Ala Pro Gly Lys Gly Leu His Glu Met Val Gly Val Lys Pro
 565 570

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 <213> Bacillus subtilis

<220>
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 aac cag atc aac agt cta ttc aaa aaa agt cat tac aac att gaa agc 20
 Asn Arg Ile Thr Gly Leu Phe Thr Lys Arg His Tyr Asn Ile Glu Ser
 25 30 35 40
 att aca att aga cag aca tta aca ttc ttc att tcc aca att att tta 45
 Ile Thr Val Gly His Thr Ala Thr Ala Gly Val Ser Arg Ile Thr Phe
 45 50 55 60
 tta att cat att tta tta tta tta tta tta tta tta tta tta tta tta 100
 Val Val His Val Glu Gly Glu Asn Asn Val Glu Glu Leu Thr Lys Glu
 105 110 115 120 125 130 135 140 145 150

51	55	60	
ctc aac aaa sag att gat gtg ctg aaa gtc aca gac atc aca aat caa	240		
Leu Asn Lys Gln Ile Asp Val Leu Lys Val Thr Asp Ile Thr Asn Gln			
65 70 75 80			
tcg att gtc sag agg gag ctg ggc tta atc aag gtt gtc tcc gca cct	288		
Ser Ile Val Gln Arg Glu Leu Ala Leu Ile Lys Val Val Ser Ala Pro			
85 90 95			
tca aca aga aca gag att aat gga atc ata gaa ccg ttt aga gac tat	336		
Ser Thr Arg Thr Glu Ile Asn Gly Ile Ile Glu Pro Phe Arg Ala Ser			
100 105 110			
gtc gtt gat gtc agc aga gac agc atc gtt gtt sag ggc aca ggt gaa	384		
Val Val Asp Val Ser Arg Asp Ser Ile Val Val Gln Val Thr Gly Glu			
115 120 125			
tct aac aaa att gaa gcg ctt att gag tta tta aaa cct tat ggc att	432		
Ser Asn Lys Ile Glu Ala Leu Ile Glu Leu Leu Lys Pro Tyr Gly Ile			
130 135 140			
aaa gaa atc gcg aga aca ggt aca acg gct ttt gcg agg gga acc agc	480		
Lys Glu Ile Ala Arg Thr Gly Thr Thr Ala Phe Ala Arg Gly Thr Ser			
145 150 155 160			
aaa agg cgt cat cca ata aaa caa tat ata ttg tat aaa aca taa	528		
Lys Arg Arg His Pro Ile Lys Gln Tyr Leu Leu Tyr Lys Thr			
165 170			

<210> 34
 <211> 174
 <212> FRT
 <213> Bacillus subtilis

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 20 25 30
 Ile Thr Val Gly His Thr Gln Thr Ala Gly Val Ser Arg Ile Thr Phe
 35 40 45
 Val Val His Val Gln Gly Gln Asn Asp Val Gln Gln Leu Thr Lys Gln
 50 55 60
 Leu Asn Lys Gln Ile Asp Val Leu Lys Val Thr Asp Ile Thr Asn Gln
 65 70 75 80
 Ser Ile Val Gln Arg Gln Leu Ala Leu Ile Lys Val Val Ser Ala Pro
 85 90 95
 Ser Thr Arg Thr Gln Ile Asn Gly Ile Ile Gln Ile Phe Arg Ala Ser
 100 105 110 115
 Val Val Asp Val Ser Arg Asp Ser Ile Val Val Gln Val Thr Gly Gln
 120 125 130

Lys Arg Arg His Pro Ile Lys Gln Tyr Leu Leu Tyr Lys Thr
165 170

K4009 35															
atg gta aaa gta tat tat aac ggt gat atc aaa gag aac gla ttg gct	48														
Met Val Lys Val Tyr Tyr Asn Gly Asp Ile Lys Glu Asn Val Leu Ala															
1 5 10 15															
gga aaa acc gta gcg gtt atc ggg tac ggt tcc caa gcc cac gca cat	96														
Gly Lys Thr Val Ala Val Ile Gly Tyr Gly Ser Gln Gly His Ala His															
20 25 30															
gcc ctc aac att aaa gaa agc gga gta gac gtg atc gtc ggt gtt aga	144														
Ala Leu Asn Leu Lys Glu Ser Gly Val Asp Val Ile Val Gly Val Arg															
35 40 45															
cac gga aaa ttt ttc act caa gcc caa gaa gac gga cat aaa gta ttt	192														
Gln Gly Lys Ser Phe Thr Gln Ala Gln Glu Asp Gly His Lys Val Phe															
50 55 60															
tca ata aaa gaa gcg gca gcc caa gcc gaa atc atc atc gtt ctg ctc	240														
Ser Val Lys Glu Ala Ala Ala Gln Ala Glu Ile Ile Met Val Leu Leu															
65 70 75 80															
cgc gat gag cag cag caa caa gta tac gaa gcc gaa atc aac gat gaa	288														
Phe Asp Gln Gln Gln Gln Lys Val Tyr Glu Ala Glu Ile Lys Asp Gln															
85 90 95															
ttg acc gca aga aaa tca tta gta ttc gcc cat gaa ttt aac ttg cat	336														
Leu Thr Ala Gly Lys Ser Leu Val Phe Ala His Glu Phe Asn Val His															
100 105 110															
ttt cat caa att att tat tgg gcg gat gta gat gta ttc tta gtg gcc	384														
Phe His Gln Ile Val Pro Pro Ala Asp Val Asp Val Phe Leu Val Ala															
115 120 125															
cat aaa att att gga caa ttt gta aca gga acc acc tat gag caa gta gct	432														
Phe Lys Gly Phe Gly His Leu Val Arg Arg Thr Tyr Gln Gln Gly Ala															
130 135 140															
att ata att ata ttg ttt tta atc tat taa att gta att gta att gta	480														
Gly Val Phe Ala Leu Phe Ala Ile Tyr Glu Asp Val Thr Val Thr Val Ala															
145 150 155															
ata ttc acc att ttc ttc ttc ttc ttc gaa tta att att att att att att	528														
Ala Phe Acc Ile Ile Ile Ile Ile Ile Ile Ile Ile Ile Ile Ile Ile Ile															
160 165 170 175 180 185 190															

Arg	Asp	Lys	Ala	Leu	Ala	Tyr	Ala	Lys	Gly	Ile	Gly	Gly	Ala	Arg	Ala	
				165					170					175		
ggc	gta	tta	gaa	acg	aca	ttt	aaa	gaa	gaa	aca	gaa	aca	gat	ttg	tto	576
Gly	Val	Leu	Glu	Thr	Thr	Phe	Lys	Glu	Glu	Thr	Glu	Thr	Asp	Leu	Phe	
			180					185					190			
ggg	gag	caa	gca	gtt	ctt	tgc	ggc	gga	tta	agg	ggg	ctt	gtc	aaa	goc	624
Gly	Glu	Gln	Ala	Val	Leu	Cys	Gly	Gly	Leu	Ser	Ala	Leu	Val	Lys	Ala	
		195					200					205				
gga	ttt	gaa	acc	tta	act	gaa	gca	ggg	tat	cag	ctt	gaa	ctt	gca	tac	672
Gly	Phe	Glu	Thr	Leu	Thr	Glu	Ala	Gly	Tyr	Gln	Pro	Glu	Leu	Ala	Tyr	
	210					215				220						
ttc	gag	tgt	ctt	cat	gag	ctg	aaa	tta	atc	gta	gac	ctt	atg	tac	gaa	720
Phe	Glu	Cys	Leu	His	Glu	Leu	Lys	Leu	Ile	Val	Asp	Leu	Met	Tyr	Glu	
225					230				235						240	
gaa	gga	ctt	gca	gga	atg	aga	tat	tca	atc	tct	gac	aca	gca	cag	tgg	768
Glu	Gly	Leu	Ala	Gly	Met	Arg	Tyr	Ser	Ile	Ser	Asp	Thr	Ala	Gln	Trp	
			245						250					255		
gga	gat	tto	gta	tca	ggc	ctt	cgc	gtt	gtg	gac	gcc	aaa	gta	aaa	gaa	816
Gly	Asp	Phe	Val	Ser	Gly	Pro	Arg	Val	Val	Asp	Ala	Lys	Val	Lys	Glu	
			260					265					270			
tct	atg	aaa	gaa	gta	tta	aaa	gat	atc	caa	aac	ggg	aca	tto	gca	aaa	864
Ser	Met	Lys	Glu	Val	Leu	Lys	Asp	Ile	Gln	Asn	Gly	Thr	Phe	Ala	Lys	
		275					280					285				
gag	tgg	atc	gtc	gaa	aac	caa	gta	aac	cgt	ctt	cgt	tto	aac	ggt	atc	912
Glu	Trp	Ile	Val	Glu	Asn	Gln	Val	Asn	Arg	Pro	Arg	Phe	Asn	Ala	Ile	
	290					295					300					
aat	gca	agc	gag	aac	gaa	cat	caa	atc	aaa	gta	gtg	gga	aga	aag	ctt	960
Asn	Ala	Ser	Glu	Asn	Glu	His	Gln	Ile	Glu	Val	Val	Gly	Arg	Lys	Leu	
305				310					315						320	
cgt	gaa	atg	atg	cgc	ttt	gtg	aaa	caa	ggc	aag	aag	aag	gaa	ggg	gtg	1008
Arg	Glu	Met	Met	Pro	Phe	Val	Lys	Gln	Gly	Lys	Lys	Lys	Glu	Ala	Val	
				325				330					335			
gtc	tcc	glt	gag	caa	aat	taa										1024
Val	Ser	Val	Ala	Gln	Asn											
			340													
<210>	36															
<211>	342															
<212>	FRT															
<213>	Bacillus subtilis															
<401>	36															
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Gly	Lys	Thr	Val	Ala	Val	Ile	Gly	Tyr	Gly	Ser	Gln	Gly	His	Ala	His	
Ala	Leu	Asn	Leu	Lys	Gln	Ser	Gly	Val	Asp	Val	Ile	Val	Gly	Val	Arg	

35						40						45					
Gln	Gly	Lys	Ser	Phe	Thr	Gln	Ala	Gln	Glu	Asp	Gly	His	Lys	Val	Phe		
50						55					60						
Ser	Val	Lys	Glu	Ala	Ala	Ala	Gln	Ala	Glu	Ile	Ile	Met	Val	Leu	Leu		
65					70					75					80		
Pro	Asp	Glu	Gln	Gln	Gln	Lys	Val	Tyr	Glu	Ala	Glu	Ile	Lys	Asp	Glu		
				85					90					95			
Leu	Thr	Ala	Gly	Lys	Ser	Leu	Val	Phe	Ala	His	Gly	Phe	Asn	Val	His		
			100					105					110				
Phe	His	Gln	Ile	Val	Pro	Pro	Ala	Asp	Val	Asp	Val	Phe	Leu	Val	Ala		
		115					120					125					
Pro	Lys	Gly	Pro	Gly	His	Leu	Val	Arg	Arg	Thr	Tyr	Glu	Gln	Gly	Ala		
		130					135				140						
Gly	Val	Pro	Ala	Leu	Phe	Ala	Ile	Tyr	Gln	Asp	Val	Thr	Gly	Glu	Ala		
145					150					155					160		
Arg	Asp	Lys	Ala	Leu	Ala	Tyr	Ala	Lys	Gly	Ile	Gly	Gly	Ala	Arg	Ala		
				165					170					175			
Gly	Val	Leu	Glu	Thr	Thr	Phe	Lys	Glu	Glu	Thr	Glu	Thr	Asp	Leu	Phe		
			180					185					190				
Gly	Glu	Gln	Ala	Val	Leu	Cys	Gly	Gly	Leu	Ser	Ala	Leu	Val	Lys	Ala		
		195					200						205				
Gly	Phe	Glu	Thr	Leu	Thr	Glu	Ala	Gly	Tyr	Gln	Pro	Glu	Leu	Ala	Tyr		
		210					215				220						
Phe	Gln	Cys	Leu	His	Glu	Leu	Lys	Leu	Ile	Val	Asp	Leu	Met	Tyr	Glu		
225					230					235					240		
Glu	Gly	Leu	Ala	Gly	Met	Arg	Tyr	Ser	Ile	Ser	Asp	Thr	Ala	Gln	Trp		
				245					250					255			
Gly	Asp	Phe	Val	Ser	Gly	Pro	Arg	Val	Val	Asp	Ala	Lys	Val	Lys	Glu		
			260					265					270				
Ser	Met	Lys	Glu	Val	Leu	Lys	Asp	Ile	Gln	Asn	Gly	Thr	Phe	Ala	Lys		
		275					280						285				
Glu	Trp	Ile	Val	Glu	Asn	Gln	Val	Asn	Arg	Pro	Arg	Phe	Asn	Ala	Ile		
		290			295						300						
Asn	Ala	Ser	Glu	Asn	Glu	His	Gln	Ile	Glu	Val	Val	Gly	Arg	Lys	Leu		
305					310					315					320		
Arg	Glu	Met	Met	Pro	Phe	Val	Lys	Gln	Gly	Lys	Lys	Lys	Glu	Ala	Val		
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Val	Ser	Val	Ala	Gln	Asn												
				34													

<211> 1674

<212> DNA

<213> Bacillus subtilis

<220>

<221> CDS

<222> (1)...(1674)

<400> 37

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Met	Ala	Glu	Leu	Arg	Ser	Asn	Met	Ile	Thr	Gln	Gly	Ile	Asp	Arg	Ala	
1				5				10					15			

arg	aac	cgc	agt	ttg	ctt	cgt	gca	gca	ggg	gta	aaa	gaa	gag	gat	ttc	96
Pro	His	Arg	Ser	Leu	Leu	Arg	Ala	Ala	Gly	Val	Lys	Glu	Glu	Asp	Phe	
			20				25					30				

ggc	aag	cag	ttt	att	gag	gtg	tgt	aat	tca	tac	att	gat	atc	gtt	ccc	144
Gly	Lys	Pro	Phe	Ile	Ala	Val	Cys	Asn	Ser	Tyr	Ile	Asp	Ile	Val	Pro	
		35				40						45				

ggc	cat	gtt	cac	ttg	cag	gag	ttt	ggg	aaa	atc	gta	aaa	gaa	gca	atc	192
Gly	His	Val	His	Leu	Gln	Glu	Phe	Gly	Lys	Ile	Val	Lys	Glu	Ala	Ile	
	50					55				60						

aga	gaa	gca	ggg	ggc	gtt	cag	ttt	gaa	ttt	aat	acc	att	ggg	gta	gat	240
Arg	Glu	Ala	Gly	Gly	Val	Pro	Phe	Glu	Phe	Asn	Thr	Ile	Gly	Val	Asp	
65					70					75					80	

gat	ggc	atc	gca	atg	ggg	cat	atc	ggt	atg	aga	tat	tgc	ctg	cca	agc	288
Asp	Gly	Ile	Ala	Met	Gly	His	Ile	Gly	Met	Arg	Tyr	Ser	Leu	Pro	Ser	
				85				90						95		

cgt	gaa	att	atc	gca	gac	tct	gtg	gaa	acg	gtt	gta	tca	gca	aac	tgg	336
Arg	Glu	Ile	Ile	Ala	Asp	Ser	Val	Glu	Thr	Val	Val	Ser	Ala	His	Trp	
		100					105					110				

ttt	gac	gga	atg	gtc	tgt	att	cag	aac	tgc	gac	aaa	atc	aca	cag	gga	384
Phe	Asp	Gly	Met	Val	Cys	Ile	Pro	Asn	Cys	Asp	Lys	Ile	Thr	Pro	Gly	
		115				120						125				

atg	ctt	atg	gag	gca	atg	cgc	atc	aac	att	cag	acg	att	ttt	gtc	agc	432
Met	Leu	Met	Ala	Ala	Met	Arg	Ile	Asn	Ile	Pro	Thr	Ile	Phe	Val	Ser	
	130					135					140					

ggc	gga	cag	atg	gag	gca	gga	aga	aca	agt	tac	ggg	cga	aaa	atc	tcc	480
Gly	Gly	Pro	Met	Ala	Ala	Gly	Arg	Thr	Ser	Tyr	Gly	Arg	Lys	Ile	Ser	
145				150				155						160		

ttt	tcc	tca	gta	ttc	gaa	ggg	gta	ggt	ggt	tac	caa	gca	ggt	aaa	atc	528
Leu	Ser	Ser	Val	Phe	Glu	Gly	Val	Gly	Ala	Tyr	Gln	Ala	Gly	Lys	Ile	
			165				170						175			

aac	gaa	aac	gag	ctt	cac	gaa	gta	aat	cag	tcc	gga	tcc	cca	aat	tcc	576
Asn	Glu	Asn	Glu	Leu	Gln	Glu	Leu	Gln	Gln	Phe	Gly	Lys	Pro	Thr	Cys	
			180				185						190			

ggt	ctt	ctt	tca	agt	atc	ttt	att	ttt	aac	tca	att	aat	tcc	ctt	tca	624
Gly	Ser	Gly	Ser	Gly	Met	Phe	Thr	Ala	Asn	Ser	Met	Asn	Gly	Leu	Ser	
		195					200						205			

gaa	gaa	ctt	ggt	ctt	ggt	ttg	cgg	ggt	aat	gga	acc	att	ctg	gca	aca	672
Glu	Ala	Leu	Gly	Leu	Ala	Leu	Pro	Gly	Asn	Gly	Thr	Ile	Leu	Ala	Thr	
210						215					220					
tct	cgg	gaa	cgt	aaa	gag	ttt	gtg	aga	aaa	tgg	ggt	gag	caa	tta	atg	720
Ser	Pro	Glu	Arg	Lys	Glu	Phe	Val	Arg	Lys	Ser	Ala	Ala	Gln	Leu	Met	
225					230					235					240	
gaa	acg	att	cgc	aaa	gat	atc	aaa	cgg	cgt	gat	att	ggt	aca	gta	aaa	768
Glu	Thr	Ile	Arg	Lys	Asp	Ile	Lys	Pro	Arg	Asp	Ile	Val	Thr	Val	Lys	
				245					250					255		
gcg	att	gat	aac	gog	ttt	gca	ctc	gat	atg	gog	ctc	gga	ggt	tct	aca	816
Ala	Ile	Asp	Asn	Ala	Phe	Ala	Leu	Asp	Met	Ala	Leu	Gly	Gly	Ser	Thr	
			260					265					270			
aat	acc	gtt	ctt	cat	acc	ctt	gac	ctt	aca	aac	gaa	gac	ggt	gtt	gaa	864
Asn	Thr	Val	Leu	His	Thr	Leu	Ala	Leu	Ala	Asn	Glu	Ala	Gly	Val	Glu	
		275					280					285				
tac	tct	tta	gaa	cgc	att	aac	gaa	gtc	gct	gag	cgc	gtg	cgg	cac	ttg	912
Tyr	Ser	Leu	Glu	Arg	Ile	Asn	Glu	Val	Ala	Glu	Arg	Val	Pro	His	Leu	
	290					295					300					
ggt	aag	ctg	gog	cct	gca	tgg	gat	gtg	ttt	att	gaa	gat	ctt	aac	gaa	960
Ala	Lys	Leu	Ala	Pro	Ala	Ser	Asp	Val	Phe	Ile	Glu	Asp	Leu	His	Glu	
305					310					315					320	
gag	ggc	ggt	gtt	tca	gog	gct	ctg	aat	gag	ctt	tgg	aag	aaa	gaa	gga	1008
Ala	Gly	Gly	Val	Ser	Ala	Ala	Leu	Asn	Glu	Leu	Ser	Lys	Lys	Glu	Gly	
				325				330						335		
gog	ctt	cat	tta	gat	gog	ctg	act	gtt	aca	gga	aaa	act	ctt	gta	gaa	1056
Ala	Leu	His	Leu	Asp	Ala	Leu	Thr	Val	Thr	Gly	Lys	Thr	Leu	Gly	Glu	
			340				345						350			
aat	att	gac	gga	cat	gaa	gta	aag	gat	tat	gac	gtc	att	cac	cgg	ctg	1104
Thr	Ile	Ala	Gly	His	Glu	Val	Lys	Asp	Tyr	Asp	Val	Ile	His	Pro	Leu	
		355					360					365				
gat	caa	cga	tta	act	gaa	aag	gga	ggt	att	gct	atc	tta	ctc	ggt	aat	1152
Asp	Gln	Pro	Phe	Thr	Glu	Lys	Gly	Gly	Leu	Ala	Val	Leu	Phe	Gly	Asn	
	370					375					380					
cta	gct	cgg	gac	ggc	gct	atc	att	aaa	aca	ggc	ggc	gta	cag	aat	ggg	1200
Leu	Ala	Pro	Asp	Gly	Ala	Ile	Ile	Lys	Thr	Gly	Gly	Val	Gln	Asn	Gly	
385					390					395					400	
att	aca	aga	cat	gaa	ggg	cgg	act	gtr	gta	tta	gat	tct	caa	gac	gag	1248
Ile	Thr	Arg	His	Glu	Gly	Pro	Ala	Val	Val	Phe	Asp	Ser	Gln	Asp	Gln	
			405					410						415		
ggt	ctt	gac	ggc	att	atc	aac	cga	aaa	gta	aaa	gaa	ggt	gac	att	gtt	1296
Ala	Leu	Asp	Gly	Ile	Ile	Asn	Arg	Lys	Val	Lys	Gln	Gly	Asp	Val	Val	
			42				425						430			
att	atc	gaa	tta	gaa	ggt	cga	aaa	ggt	gta	tta	gat	tct	caa	gac	gag	1344
Ile	Ile	Arg	Tyr	Gln	Gly	Pro	Lys	Gly	Gly	Phe	Gly	Met	Phe	Gln	Met	
		435				44						445				
cta	gct	cgg	gac	ggc	gct	atc	att	aaa	aca	ggc	ggc	gta	cag	aat	ggg	1392
Leu	Ala	Pro	Asp	Gly	Ala	Ile	Ile	Lys	Thr	Gly	Gly	Val	Gln	Asn	Gly	
395					390					395					400	

Leu Ala Pro Thr Ser Gln Ile Val Gly Met Gly Leu Gly Pro Lys Val
450 455 460

gga ttg att acg gac gga cgt ttt tcc gga ggc tcc cgt ggc tcc tca 1440
Ala Leu Ile Thr Asp Gly Arg Phe Ser Gly Ala Ser Arg Gly Leu Ser
465 470 475 480

atc ggc cac gta tca cct gag gac gat gag ggc ggg cgg ctt ggc ttt 1488
Ile Gly His Val Ser Pro Glu Ala Ala Glu Gly Gly Pro Leu Ala Phe
485 490 495

gtt gaa aac gga gac cat att atc gtt gat att gaa aaa cgc atc ttg 1536
Val Glu Asn Gly Asp His Ile Ile Val Asp Ile Glu Lys Arg Ile Leu
500 505 510

gat gta caa gtg cca gaa gaa gag tgg gaa aaa cga aaa ggc aac tgg 1584
Asp Val Gln Val Pro Glu Glu Glu Trp Glu Lys Arg Lys Ala Asn Trp
515 520 525

aaa ggt ttt gaa cgg aaa gtg aaa acc ggc tac ctg gca cgt tat tct 1632
Lys Gly Phe Glu Pro Lys Val Lys Thr Gly Tyr Leu Ala Arg Tyr Ser
530 535 540

aaa ctt gtg aca agt ggc aac acc ggc ggt att atg aaa atc 1674
Lys Leu Val Thr Ser Ala Asn Thr Gly Gly Ile Met Lys Ile
545 550 555

<210> 38

<211> 558

<212> PRT

<213> Bacillus subtilis

<400> 38

Met Ala Gln Leu Arg Ser Asn Met Ile Thr Gln Gly Ile Asp Arg Ala
1 5 10 15

Pro His Arg Ser Leu Leu Arg Ala Ala Gly Val Lys Glu Glu Asp Phe
20 25 30

Gly Lys Pro Phe Ile Ala Val Cys Asn Ser Tyr Ile Asp Ile Val Pro
35 40 45

Gly His Val His Leu Gln Glu Phe Gly Lys Ile Val Lys Glu Ala Ile
50 55 60

Arg Glu Ala Gly Gly Val Pro Phe Gln Phe Asn Thr Ile Gly Val Asp
65 70 75

Asp Gly Ile Ala Met Gly His Ile Gly Met Arg Tyr Ser Leu Pro Ser
85 90 95

Arg Glu Ile Ile Ala Asp Ser Val Gln Thr Val Val Ser Ala His Trp
100 105 110

Phe Asp Gly Met Val Cys Ile Pro Asn Lys Asp Lys Ile Thr Pro Gly
115 120 125

Met Leu Met Ala Ala Met Arg Ile Asn Ile Pro Thr Ile Ile Val Ser
130 135 140

Gly 145	Gly	Pro	Met	Ala	Ala 150	Gly	Arg	Thr	Ser	Tyr 155	Gly	Arg	Lys	Ile	Ser 160
Leu	Ser	Ser	Val	Phe 165	Glu	Gly	Val	Gly	Ala 170	Tyr	Gln	Ala	Gly	Lys 175	Ile
Asn	Glu	Asn	Glu 180	Leu	Gln	Glu	Leu	Glu 185	Gln	Phe	Gly	Cys	Pro 190	Thr	Cys
Gly	Ser	Cys 195	Ser	Gly	Met	Phe	Thr 200	Ala	Asn	Ser	Met	Asn 205	Cys	Leu	Ser
Glu 210	Ala	Leu	Gly	Leu	Ala	Leu 215	Pro	Gly	Asn	Gly	Thr 220	Ile	Leu	Ala	Thr
Ser 225	Pro	Glu	Arg	Lys	Glu 230	Phe	Val	Arg	Lys	Ser 235	Ala	Ala	Gln	Leu	Met 240
Glu	Thr	Ile	Arg	Lys 245	Asp	Ile	Lys	Pro	Arg 250	Asp	Ile	Val	Thr	Val 255	Lys
Ala	Ile	Asp	Asn 260	Ala	Phe	Ala	Leu	Asp 265	Met	Ala	Leu	Gly	Gly 270	Ser	Thr
Asn	Thr	Val	Leu	His 275	Thr	Leu	Ala 280	Leu	Ala	Asn	Glu	Ala 285	Gly	Val	Glu
Tyr 290	Ser	Leu	Glu	Arg	Ile	Asn 295	Glu	Val	Ala	Glu	Arg 300	Val	Pro	His	Leu
Ala 305	Lys	Leu	Ala	Pro	Ala 310	Ser	Asp	Val	Phe	Ile 315	Glu	Asp	Leu	His	Glu 320
Ala	Gly	Gly	Val 325	Ser	Ala	Ala	Leu	Asn 330	Glu	Leu	Ser	Lys	Lys	Glu 335	Gly
Ala	Leu	His	Leu 340	Asp	Ala	Leu	Thr	Val 345	Thr	Gly	Lys	Thr	Leu 350	Gly	Glu
Thr	Ile	Ala	Gly 355	His	Glu	Val	Lys 360	Asp	Tyr	Asp	Val	Ile 365	His	Pro	Leu
Asp 370	Gln	Pro	Phe	Thr	Glu 375	Lys	Gly	Gly	Leu	Ala	Val 380	Leu	Phe	Gly	Asn
Leu 385	Ala	Pro	Asp	Gly	Ala 390	Ile	Ile	Lys	Thr	Gly 395	Gly	Val	Gln	Asn	Gly 400
Ile	Thr	Arg	His 405	Glu	Gly	Pro	Ala	Val 410	Val	Phe	Asp	Ser	Gln	Asp 415	Glu
Ala	Leu	Asp	Gly 420	Ile	Ile	Asn	Arg	Lys 425	Val	Lys	Glu	Gly	Asp 430	Val	Val
Ile	Ile	Arg	Tyr 435	Glu	Gly	Pro	Lys 440	Gly	Gly	Pro	Gly	Met 445	Pro	Gln	Met
Leu 450	Ala	Pro	Thr	Ser	Gln 455	Ile	Val	Gly	Met	Gly	Leu 460	Gly	Pro	Lys	Val
Ala	Leu	Ile	Thr	Asp	Gly	Arg	Ile	Ser	Gly	Ala	Ser	Arg	Gly	Leu	Ser

the β phase of the polymer. The β phase is the more ordered phase and is characterized by a higher density and a higher melting point than the α phase. The β phase is also the more stable phase and is the one that is most commonly observed in nature. The α phase is the less ordered phase and is characterized by a lower density and a lower melting point than the β phase. The α phase is also the less stable phase and is the one that is most commonly observed in nature.

<400> 40
 gctacctag ctcccaagaa agatatacta acagcacaag aggggaaaga tgttttgctc 60
 tacatccaga acaacctctg ctaaaattcc tgaaaaattt tgcaaaaagt tgttgacttt 120
 atctacaagg tgtggtataa taatottaac aacagcagga cgc 163

<210> 41
 <211> 127
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:promoter
 sequence

<220>
 <221> -35_signal
 <222> (34)..(39)

<220>
 <221> -10_signal
 <222> (58)..(63)

<220>
 <221> -35_signal
 <222> (75)..(80)

<220>
 <221> -10_signal
 <222> (98)..(103)

<400> 41
 gaggatcat agaattttgt caaaataatt ttattgaca agtcttata agtgatat 60
 aatttaatt ttattgaca aaaatgggt cgtgttgtac aataaatgta gtgaggcgga 120
 tgcactg 127

<210> 42
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:ribosome
 binding site

<400> 42
 taacatgag gaggagaaa catg 34

<210> 43
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:ribosome

binding site

<400> 43
attcgagaaa tggagagaat ataatatg

28

<210> 44
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ribosome
binding site

<400> 44
agaaaggagg tga

13

<210> 45
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ribosome
binding site

<210>
<211> misc_feature
<222> 17-20
<223> n = a, c, g, or t

<400> 45
ttaaqaaggagg aggtgannnn atg

23

<210> 46
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ribosome
binding site

<210>
<211> misc_feature
<222> 16-27
<223> n = a, c, g, or t

<400> 46
ttaaaaagga ggtgannnnn atg

23

<210> 47
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ribosome
binding site

<220>

<221> misc_feature

<222> 14-20

<223> n = a, c, g, or t

<400> 47

agaaaggagg tgannnnnnn atg

23

<210> 48

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:ribosome
binding site

<220>

<221> misc_feature

<222> 14-19

<223> n = a, c, g, or t

<400> 48

agaaaggagg tgannnnnna tg

22

<210> 49

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:ribosome
binding site

<400> 49

ccctctadag gaggagana acatg

25

<210> 50

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:ribosome
binding site

<400> 50

ccctctadag gaggagana catg

24

<210> 51

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:ribosome
binding site

<400> 51

ccctctadag gaggagana atg

24

<210> 51
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ribosome
binding site

<400> 52
ttagaaagga ggtttaatta atg

23

<210> 53
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ribosome
binding site

<400> 53
ttagaaagga ggtgatttaa atg

23

<210> 54
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ribosome
binding site

<400> 54
ttagaaagga ggtgttataa atg

23

<210> 55
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ribosome
binding site

<400> 55
attcagagaaa ggaagtgaaat ataatatg

28

<210> 56
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:ribosome
binding site

<400> 56
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<210> 57

<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: ribosome
binding site

<400> 57
atcgttagaa aggaggtyaa ttaatatg

25

<210> 58
<211> 3291
<212> DNA
<213> Bacillus subtilis

<400> 58
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gcattaatgc tgattgaatc attaaaaaaa gagaaagtag aaatgatott cggttatocg 120
ggcgggggtg tgottocgat ttaagataag ctatacaatt cagggttggg acatatcatt 180
cccggtcagc aacaaggagc aattcagca gcggagggat accgaaggtt ctcggaaaa 240
ccgggtgtcg taattgcac gtcaggggcg ggagcgacaa accttgtnac aggcottggt 300
gatgcacga ttgattcaat gcggttagtc gtccttacag ggcaggtajc aacctctgta 360
atcgggagcg atgcatttca ggaagcagac attctagga ttacgatgac agtcaaaaa 420
cacagctatc aggttcgcac gcgggaagat ctgagcgca tcaaaaaa agcgttcac 480
attcaaaaa ctggaagatc cggacgtga ttgatgata ttcgaaaaa cgtagcaaca 540
attgaaggag aattcagctc cgatcatgag atgaatcttc cgggatacca gcgcacaaca 600
gagcogaatt atttcagat ccgcaagctt gtggaagcgc tgagcagtg caaaaaacgc 660
gtgatcttg cgggtgcggg cgtactgcac gaaaaacgt cagaagaatt aaaaaattat 720
gtggaacagc agcaaatccc tctggcacac acctttctg ggtcggagg attccgggt 780
aacatccgc tttctctagg gctggcgga atgcacgca ctatadaca caatatac 840
ctaatgaat gtgatctat aattagtat cccacacat ttgagacg tgcacagga 900
aacctgaaa accttgccag aaacgaaa ataacccaa tcatattc tccactcaa 960
atcgaaaaa tcatgaaa acatattc gtactggga acatgaaa tgcctgcac 1020
gactatca aacagaaa caaaaaaa gattcaggt aatgaaaa acatctca 1080
gactgaaa gactatca cctcctat ctactatc aaaaaa atttattc 1140
ctactatg ctgactat ctactatc aaaaaa agctatgt cctactat 1200
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gtcaagtcag gaggacttgg aagcatggga ttgggttttc aggcggcgat cggcgccacag 1320
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 cagaggggatg aaactcgccg aactttagaa agtgaagaat ccttctcggt gtaacgggaag 180
 gttcttttgc ttgcagaaag aaacgggcaga tcatctcttc caaacatgag taagaaaaa 240
 c atg aaa aca aaa ctg gat ttt cta aaa atg aag gag tct gaa gaa cag 289
 Met Lys Thr Lys Leu Asp Phe Leu Lys Met Lys Glu Ser Glu Glu Pro
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att gtc atg ctg acc gct tat gat tat ccg gca gct aaa ctt acg gaa 337
 Ile Val Met Leu Thr Ala Tyr Asp Tyr Pro Ala Ala Lys Leu Ala Glu
 20 25 30

caa ccg gga gtt gac atg att tta gtc ggt gat tca ctt gga atg gtc 385
 Gln Ala Gly Val Asp Met Ile Leu Val Gly Asp Ser Leu Gly Met Val
 35 40 45

gta ctc ggc ctt gat tca act gta att atg aaa gtt ccg gac atg atc 433
 Val Leu Gly Leu Asp Ser Thr Val Gly Val Thr Val Ala Asp Met Ile
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cat cat aca aaa gcc gtt aaa aga ggt ggc cca att acc ttt att ata 481
 His His Thr Lys Ala Val Lys Arg Gly Ala Pro Asn Thr Phe Ile Val
 65 70 75

aca gat att cca ttt att tct tat cac ctt tct aag gaa att att att 529
 Thr Asp Met Phe Phe Met Ser Tyr His Leu Ser Lys Glu Asp Thr Leu
 80 85 90

aaa att att att gtt att att agc gaa att att att att att att att 577
 Lys Asn Ala Ala Ala Ile Val Glu Glu Ser Gly Ala Asp Ala Leu Lys
 95 100 105

ctt	gag	ggc	gga	gaa	ggc	gtg	ttt	gaa	ccc	att	ggc	gca	ttg	acg	ctt	625
Leu	Glu	Gly	Gly	Glu	Gly	Val	Phe	Glu	Ser	Ile	Arg	Ala	Leu	Thr	Leu	
		113					120					123				
gga	ggc	att	aca	gta	gtc	agt	cac	tta	ggc	ttg	aca	cag	cag	tca	gtc	673
Gly	Gly	Ile	Pro	Val	Val	Ser	His	Leu	Gly	Leu	Thr	Pro	Gln	Ser	Val	
	130					135					140					
ggc	gta	ctg	ggc	ggc	tat	aaa	gta	cag	ggc	aaa	gac	gaa	caa	agc	ggc	721
Gly	Val	Leu	Gly	Gly	Tyr	Lys	Val	Gln	Gly	Lys	Asp	Glu	Gln	Ser	Ala	
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Lys	Lys	Leu	Ile	Glu	Asp	Ser	Ile	Lys	Cys	Glu	Glu	Ala	Gly	Ala	Met	
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Asp	Gly	Gln	Val	Leu	Val	Tyr	His	Asp	Ile	Ile	Gly	His	Gly	Val	Glu	
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Glu	Thr	Ala	Ile	Ser	Gly	Tyr	Val	Gln	Asp	Val	Arg	His	Arg	Ala	Phe	
			245					250					255			
ccc	gaa	caa	aag	cat	ccc	ttt	caa	atg	aac	cag	aca	gtg	ctt	gac	ggc	1057
Pro	Glu	Gln	Lys	His	Ser	Phe	Gln	Met	Asn	Gln	Thr	Val	Leu	Asp	Gly	
			260					265					270			
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Leu	Tyr	Gly	Gly	Lys		Met	Arg	Gln	Ile	Thr	Asp	Ile	Ser	Gln	Leu	
		275						280					285			
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Lys	Glu	Ala	Ile	Lys	Gln	Tyr	His	Ser	Glu	Gly	Lys	Ser	Ile	Gly	Phe	
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Val	Pro	Thr	Met	Gly	Phe	Leu	His	Glu	Gly	His	Leu	Thr	Leu	Ala	Asp	
		305				310					315					
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Lys	Ala	Arg	Gln	Gln	Asp	Asp	Ala	Val	Ile	Met	Ser	Ile	Phe	Val	Asn	
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Ile	Glu	Arg	Asp	Ala	Ala	Leu	Ala	Glu	Asn	Ala	Gly	Val	Asp	Ile	Leu	
			355					360					365			
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Phe	Thr	Pro	Asp	Ala	His	Asp	Met	Tyr	Pro	Gly	Glu	Lys	Asn	Val	Thr	
		370					375					380				
att	cat	gta	gaa	aga	ggc	aca	gac	gtg	tta	tgc	ggg	ggc	tca	aga	gaa	1442
Ile	His	Val	Glu	Arg	Arg	Thr	Asp	Val	Leu	Cys	Gly	Arg	Ser	Arg	Glu	
		385				390					395					
gga	cat	ttt	gac	ggg	gtc	ggc	atc	gta	tig	aag	aag	ctt	ttc	aat	cta	1490
Gly	His	Phe	Asp	Gly	Val	Ala	Ile	Val	Leu	Thr	Lys	Leu	Phe	Asn	Leu	
400					405					410					415	
gtc	aag	ccg	aat	agt	gac	tat	ttc	ggt	tta	aaa	gat	ggc	cag	cag	gta	1538
Val	Lys	Pro	Thr	Arg	Ala	Tyr	Phe	Gly	Leu	Lys	Asp	Ala	Gln	Gln	Val	
				420				425						430		
gct	gtt	gtt	gat	ggg	tta	atc	agc	gac	ttc	ttc	atg	gat	att	gaa	tgc	1586
Ala	Val	Val	Asp	Gly	Leu	Ile	Ser	Asp	Phe	Phe	Met	Asp	Ile	Glu	Leu	
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gtt	ccg	gtc	gat	aag	gtc	aga	gag	gaa	gac	ggc	tta	gac	aaa	agg	ttt	1634
Val	Pro	Val	Asp	Thr	Val	Arg	Glu	Glu	Asp	Gly	Leu	Ala	Lys	Ser	Ser	
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ggc	aat	gta	tac	tta	aca	gct	gag	gaa	aga	aaa	gaa	ggc	ccg	aag	ctg	1682
Arg	Asn	Val	Tyr	Leu	Thr	Ala	Glu	Glu	Arg	Lys	Glu	Ala	Pro	Lys	Leu	
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tat	egg	gac	ctt	caa	aca	agt	ggc	gaa	att	gtc	caa	gac	ggt	gaa	aga	1730
Tyr	Arg	Ala	Leu	Gln	Thr	Ser	Ala	Glu	Leu	Val	Gln	Ala	Gly	Glu	Arg	
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gat	ctt	gaa	gga	gtg	ata	aaa	gct	gaa	aaa	gat	atc	att	gaa	aag	aat	1778
Asp	Pro	Glu	Ala	Val	Ile	Lys	Ala	Ala	Lys	Asp	Ile	Ile	Glu	Thr	Thr	
			500				505						510			
agg	gga	acc	ata	gac	tat	gta	gag	ctt	tat	tcc	tat	cag	gaa	ctc	gag	1826
Ser	Gly	Thr	Ile	Asp	Tyr	Val	Glu	Leu	Tyr	Ser	Tyr	Pro	Glu	Leu	Glu	
			515				520					525	530			
ccc	gtg	aat	gaa	att	gct	gga	aag	atg	att	ctc	gct	gtt	gca	gtt	gct	1874
Pro	Val	Asn	Glu	Ile	Ala	Gly	Lys	Met	Ile	Leu	Ala	Val	Ala	Val	Ala	
		535					540				545					
ttc	tca	aaa	atg	ggt	tta	ata	gat	aat	atc	att	att	gat	att	caa	gaa	1922
Phe	Ser	Lys	Ala	Arg	Leu	Ile	Asp	Asn	Ile	Ile	Ile	Asp	Ile	Arg	Glu	
	548					550				555						
atg	ggt	aga	ata	taatt	ata	tat										

Ile Asp Glu Asp Leu Ile Asp Ala Val Gly Met Leu Pro Asn Glu Lys
 595 600 605
 gta caa att gtg aat aat aat aat gga gaa cgt att gaa aag tat att 2115
 Val Gln Ile Val Asn Asn Asn Asn Gly Ala Arg Leu Glu Thr Tyr Ile
 610 615 620
 att cct ggt aaa cgg gga agc ggc gtc ata tgc tta aac ggt gca gcc 2163
 Ile Pro Gly Lys Arg Gly Ser Gly Val Ile Cys Leu Asn Gly Ala Ala
 625 630 635
 gca cgc ctt gtg cag gaa gga gat aag gtc att att att tcc tac aaa 2211
 Ala Arg Leu Val Gln Glu Gly Asp Lys Val Ile Ile Ile Ser Tyr Lys
 640 645 650
 atg atg tct gat caa gaa gcg gca agc cat gag cag aaa gtg ggt gtt 2259
 Met Met Ser Asp Gln Glu Ala Ala Ser His Glu Pro Lys Val Ala Val
 655 660 665 670
 ctg aat gat caa aac aaa att gaa caa atg ctg ggg aac gaa cca gcc 2307
 Leu Asn Asp Gln Asn Lys Ile Glu Gln Met Leu Gly Asn Glu Pro Ala
 675 680 685
 cgt aca att ttg tagaagaaaa gcccccctta cgggggggttt tcttttaaga ttat 2363
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 Asn Asp Tyr Leu Ser Val Glu Glu Val Glu Thr Ile Tyr Ile Pro Leu
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 Val Arg Leu Leu His Leu His Val Lys Ser Ala Ala Glu Arg Asn Lys
 35 40 45
 His Val Asn Val Phe Leu Lys His Pro His Ser Ala Lys Ile Pro Phe
 50 55 60
 Ile Ile Gly Ile Ala Gly Ser Val Ala Val Gly Lys Ser Thr Thr Ala
 65 70 75
 Arg Ile Leu Gln Lys Leu Leu Ser Arg Leu Pro Asp Arg Pro Lys Val
 80 85 90 95
 Ser Leu Ile Thr Thr Asp Gly Phe Leu Phe Pro Thr Ala Glu Leu Lys
 100 105 110 115
 Lys Lys Asn Met Met Ser Arg Lys Gly Phe Pro Gln Ser Tyr Asn Val
 120 125 130 135
 Lys Ala Leu Leu Glu Phe Leu Asn Asp Leu Lys Ser Gly Lys Asp Ser
 140 145 150

Val Lys Ala Pro Val Tyr Ser His Leu Thr Tyr Asp Arg Glu Glu Gly
145 150 155 160

Val Phe Glu Val Val Glu Gln Ala Asp Ile Val Ile Ile Glu Gly Ile
165 170 175

Asn Val Leu Gln Ser Pro Thr Leu Glu Asp Asp Arg Glu Asn Pro Arg
180 185 190

Ile Phe Val Ser Asp Phe Phe Asp Phe Ser Ile Tyr Val Asp Ala Glu
195 200 205

Glu Ser Arg Ile Phe Thr Trp Tyr Leu Glu Arg Phe Arg Leu Leu Arg
210 215 220

Glu Thr Ala Phe Gln Asn Pro Asp Ser Tyr Phe His Lys Phe Lys Asp
225 230 235 240

Leu Ser Asp Gln Glu Ala Asp Glu Met Ala Ala Ser Ile Trp Glu Ser
245 250 255

Val Asn Arg Pro Asn Leu Tyr Glu Asn Ile Leu Pro Thr Lys Phe Arg
260 265 270

Ser Asp Leu Ile Leu Arg Lys Gly Asp Gly His Lys Val Glu Glu Val
275 280 285

Leu Val Arg Arg Val
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<210> 61
<211> 281
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<213> Bacillus subtilis

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20 25 30

Glu Arg Asn Lys His Val Asn Val Phe Leu Lys His Pro His Ser Ala
35 40 45

Lys Ile Pro Phe Ile Ile Gly Ile Ala Gly Ser Val Ala Val Gly Lys
50 55 60

Ser Thr Thr Ala Arg Ile Leu Gln Lys Leu Leu Ser Arg Leu Pro Asp
65 70 75 80

Arg Pro Lys Val Ser Leu Ile Thr Thr Asp Gly Phe Leu Phe Pro Thr
85 90 95

Ala Glu Leu Lys Lys Lys Asn Met Met Ser Arg Lys Gly Ile Pro Glu
100 105 110

Ser Tyr Asp Val Lys Ala Leu Leu His Phe Leu Asn Asp Leu Lys Ser
115 120 125

Gly Lys Asp Ser Val Lys Ala Pro Val Tyr Ser His Leu Thr Tyr Asp
 130 135 140
 Arg Glu Glu Gly Val Phe Glu Val Val Glu Gln Ala Asp Ile Val Ile
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 Ile Glu Gly Ile Asn Val Leu Gln Ser Pro Thr Leu Glu Asp Asp Arg
 165 170 175
 Glu Asn Pro Arg Ile Phe Val Ser Asp Phe Phe Asp Phe Ser Ile Tyr
 180 185 190
 Val Asp Ala Glu Glu Ser Arg Ile Phe Thr Trp Tyr Leu Glu Arg Phe
 195 200 205
 Arg Leu Leu Arg Glu Thr Ala Phe Gln Asn Pro Asp Ser Tyr Phe His
 210 215 220
 Lys Phe Lys Asp Leu Ser Asp Gln Glu Ala Asp Glu Met Ala Ala Ser
 225 230 235 240
 Ile Trp Glu Ser Val Asn Arg Pro Asn Leu Tyr Glu Asn Ile Leu Pro
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 Thr Lys Phe Arg Ser Asp Leu Ile Leu Arg Lys Gly Asp Gly His Lys
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 Val Glu Glu Val Leu Val Arg Arg Val
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 Lys Pro Asp Pro Asn Gln Leu Ser Phe Gly Arg Val Phe Thr Asp His
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 atg ttt gta atg gac tat gcc gca gat aaa ggt tgg tac gat cca aga 144
 Met Phe Val Met Asp Tyr Ala Ala Asp Lys Gly Trp Tyr Asp Pro Arg
 35 40 45
 acc att cct tat caa ccc tta tca atg gat cca acc gca atd ggc tat 192
 Ile Ile Pro Tyr Gln Pro Leu Ser Met Asp Pro Thr Ala Met Val Tyr
 50 55 60
 tac tac agc caa acc gtc ttt gaa ggc tta aac cct tac gta tca gac 240
 His Tyr Gly Gln Thr Val Phe Gln Gly Leu Lys Ala Tyr Val Ser Glu
 65 70 75

gat	gac	cat	gtt	ctg	ctt	ttc	aga	cgg	gaa	aaa	aat	atg	gaa	cgc	ctg	288
Asp	Asp	His	Val	Leu	Leu	Phe	Arg	Pro	Glu	Lys	Asn	Met	Glu	Arg	Leu	
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aat	caa	tca	aac	gac	cgc	ctc	tgc	atc	cgg	caa	att	gat	gaa	gaa	cag	336
Asn	Gln	Ser	Asn	Asp	Arg	Leu	Cys	Ile	Pro	Gln	Ile	Asp	Glu	Glu	Gln	
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Val	Leu	Glu	Gly	Leu	Lys	Gln	Leu	Val	Ala	Ile	Asp	Lys	Asp	Trp	Ile	
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cga	aat	gcg	gag	ggc	acg	tcc	ctt	tac	atc	cgt	cgg	ttc	atc	atc	gca	432
Pro	Asn	Ala	Glu	Gly	Thr	Ser	Leu	Tyr	Ile	Arg	Pro	Phe	Ile	Ile	Ala	
	130					135					140					
acc	gag	cct	ttc	ctt	ggt	gtt	ggc	gaa	tct	cat	acg	tat	aag	ctc	tgg	480
Thr	Glu	Pro	Phe	Leu	Gly	Val	Ala	Ala	Ser	His	Thr	Tyr	Lys	Leu	Leu	
145					150					155					160	
atc	att	ctt	tct	cgg	gtc	ggc	tct	tat	tac	aaa	gaa	ggc	att	aag	cgg	528
Ile	Ile	Leu	Ser	Pro	Val	Gly	Ser	Tyr	Tyr	Lys	Glu	Gly	Ile	Lys	Pro	
			165						170					175		
gtc	aaa	atc	gat	gtt	gaa	agt	gaa	ttt	gtc	cgt	ggc	gta	aaa	ggc	gga	576
Val	Lys	Ile	Ala	Val	Glu	Ser	Glu	Phe	Val	Arg	Ala	Val	Lys	Gly	Gly	
			180					185					190			
aca	gga	aat	gac	aaa	acc	gca	gga	aac	tat	gct	tca	agc	tta	aaa	ggc	624
Thr	Gly	Asn	Ala	Lys	Thr	Ala	Gly	Asn	Tyr	Ala	Ser	Ser	Leu	Lys	Ala	
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Gln	Gln	Val	Ala	Glu	Glu	Lys	Gly	Phe	Ser	Gln	Val	Leu	Trp	Leu	Asp	
	210					215					220					
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Gly	Ile	Glu	Lys	Lys	Tyr	Ile	Glu	Glu	Val	Gly	Ser	Met	Asn	Ile	Phe	
225					230					235					240	
ttc	aaa	atc	aac	ggt	gaa	atc	gta	aca	cgg	atg	ctg	aac	ggc	agc	atc	768
Phe	Lys	Ile	Asn	Gly	Glu	Ile	Val	Thr	Pro	Met	Leu	Asn	Gly	Ser	Ile	
			245					250					255			
ctg	gaa	ggc	att	acg	cgc	aat	tca	gtc	atc	gac	ttg	ctt	aag	cat	tgg	816
Leu	Glu	Gly	Ile	Thr	Arg	Asn	Ser	Val	Ile	Ala	Leu	Leu	Lys	His	Trp	
			260					265					270			
ggc	ctt	caa	gtt	tca	gaa	cga	aaa	att	ggc	atc	gat	gag	gtc	atc	caa	864
Gly	Leu	Gln	Val	Ser	Glu	Arg	Lys	Ile	Ala	Ile	Asp	Glu	Val	Ile	Gln	
		275					280					285				
gac	cat	aaa	gac	gac	atc	ctg	gaa	gaa	gac	ttc	gga	aca	ggt	aca	gaa	912
Ala	His	Lys	Asp	Gly	Ile	Leu	Glu	Glu	Ala	Phe	Gly	Thr	Gly	Thr	Ala	
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gtt	gtt	att	tca	caa	gtc	ggc	gag	ctc	atc	tgg	caa	ggt	caa	ggt	ctt	960
Ala	Val	Ile	Ser	Pro	Val	Gly	Glu	Leu	Ile	Trp	Gln	Asp	Glu	Thr	Leu	
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tca	atc	acc	acc	gtt	caa	gaa	gaa	gaa	atc	tca	gaa	gaa	gtc	tat	gtt	1008

Ser Ile Asn Asn Gly Glu Thr Gly Glu Ile Ala Lys Lys Leu Tyr Asp
 325 330 335

acg att aca ggc att caa aaa ggc gct gtc gca gac gaa ttc gga tgg 1086
 Thr Ile Thr Gly Ile Gln Lys Gly Ala Val Ala Asp Glu Phe Gly Trp
 340 345 350

acg acc gaa gtc gca ggc ctg act gaa agc aag taa 1092
 Thr Thr Glu Val Ala Ala Leu Thr Glu Ser Lys
 355 360

<210> 63
 <211> 363
 <212> FRT
 <213> Bacillus subtilis

<400> 63
 Met Thr Lys Gln Thr Ile Arg Val Glu Leu Thr Ser Thr Lys Lys Pro
 1 5 10 15

Lys Pro Asp Pro Asn Gln Leu Ser Phe Gly Arg Val Phe Thr Asp His
 20 25 30

Met Phe Val Met Asp Tyr Ala Ala Asp Lys Gly Trp Tyr Asp Pro Arg
 35 40 45

Ile Ile Pro Tyr Gln Pro Leu Ser Met Asp Pro Thr Ala Met Val Tyr
 50 55 60

His Tyr Gly Gln Thr Val Phe Glu Gly Leu Lys Ala Tyr Val Ser Glu
 65 70 75 80

Asp Asp His Val Leu Leu Phe Arg Pro Glu Lys Asn Met Glu Arg Leu
 85 90 95

Asn Gln Ser Asn Asp Arg Leu Cys Ile Pro Gln Ile Asp Glu Glu Gln
 100 105 110

Val Leu Glu Gly Leu Lys Gln Leu Val Ala Ile Asp Lys Asp Trp Ile
 115 120 125

Pro Asn Ala Glu Gly Thr Ser Leu Tyr Ile Arg Pro Phe Ile Ile Ala
 130 135 140

Thr Glu Pro Phe Leu Gly Val Ala Ala Ser His Thr Tyr Lys Leu Leu
 145 150 155 160

Ile Ile Leu Ser Pro Val Gly Ser Tyr Tyr Lys Glu Gly Ile Lys Pro
 165 170 175

Val Lys Ile Ala Val Glu Ser Glu Phe Val Arg Ala Val Lys Gly Gly
 180 185 190

Thr Gly Asn Ala Lys Thr Ala Gly Asn Tyr Ala Ser Ser Leu Lys Ala
 195 200 205

Gln Gln Val Ala Ala Gln Lys Gly Phe Ser Gln Val Leu Trp Leu Asp
 210 215 220

Gly Ile Gln Lys Lys Tyr Ile Gln Gln Val Gly Ser Met Asn Ile Ile

225		230		235		240
Phe Lys Ile Asn Gly Glu Ile Val Thr Pro Met Leu Asn Gly Ser Ile						
		245		250		255
Leu Glu Gly Ile Thr Arg Asn Ser Val Ile Ala Leu Leu Lys His Trp						
		260		265		270
Gly Leu Gln Val Ser Glu Arg Lys Ile Ala Ile Asp Glu Val Ile Gln						
		275		280		285
Ala His Lys Asp Gly Ile Leu Glu Glu Ala Phe Gly Thr Gly Thr Ala						
		290		295		300
Ala Val Ile Ser Pro Val Gly Glu Leu Ile Trp Gln Asp Glu Thr Leu						
		305		310		315
Ser Ile Asn Asn Gly Glu Thr Gly Glu Ile Ala Lys Lys Leu Tyr Asp						
		325		330		335
Thr Ile Thr Gly Ile Gln Lys Gly Ala Val Ala Asp Glu Phe Gly Trp						
		340		345		350
Thr Thr Glu Val Ala Ala Leu Thr Glu Ser Lys						
		355		360		

<210> 64
 <211> 1071
 <212> DNA
 <213> *Bacillus subtilis*

<220>
 <221> CDS
 <222> (1)..(1068)

<400> 64	
ttg aat aag att att gaa cga gaa aaa act gta tat tat aag gaa aag	48
Met Asn Lys Leu Ile Glu Arg Glu Lys Thr Val Tyr Tyr Lys Glu Lys	
1 5 10 15	
acc gac cag tct tcc ttg ggg ttt gga caa tat ttt aca gat tat atg	96
Pro Asp Pro Ser Ser Leu Gly Phe Gly Gln Tyr Phe Thr Asp Tyr Met	
20 25 30	
ttt gtg atg gac tac gaa gag ggg att aga tgg cat cat cgg aga att	144
Phe Val Met Asp Tyr Glu Glu Gly Ile Gly Trp His His Pro Arg Ile	
35 40 45	
ggg cag tac aca cag att acg att gat cag tct tca tct gtt ttt cat	192
Ala Pro Tyr Ala Pro Leu Thr Leu Asp Pro Ser Ser Ser Val Phe His	
50 55 60	
tat ggc cag att att ttt gaa gga tta aat gta tac aca acg gac gac	240
Tyr Gly Gln Ala Val Phe Glu Gly Leu Lys Ala Tyr Arg Thr Asp Asp	
65 70 75	
ttt att ttg att att ttg ggt ggt tat caa att att aca att att att	288
Gly Arg Val Leu Leu Phe Arg Pro Asp Gln Asn Ile Lys Arg Leu Asn	
80 85 90	

aga	tgg	tgt	gag	cgc	atg	agc	atg	ccc	cct	tta	gac	gaa	gag	ctg	gtg	336
Arg	Ser	Cys	Glu	Arg	Met	Ser	Met	Pro	Pro	Leu	Asp	Glu	Glu	Leu	Val	
			100					105						110		
ctt	gag	gca	ttg	acg	caa	tta	gtt	gag	ctg	gag	aaa	gat	tgg	gtt	cca	384
Leu	Glu	Ala	Leu	Thr	Gln	Leu	Val	Glu	Leu	Glu	Lys	Asp	Trp	Val	Pro	
		115					120					125				
aag	gaa	aaa	gga	acg	tca	ctg	tat	att	cgt	cct	ttt	gtc	att	gac	aca	432
Lys	Glu	Lys	Gly	Thr	Ser	Leu	Tyr	Ile	Arg	Pro	Phe	Val	Ile	Ala	Thr	
	130					135					140					
gaa	ccg	agt	ctc	ggc	gtg	aag	gca	ccc	agg	agc	tat	aca	ttt	atg	atc	480
Glu	Pro	Ser	Leu	Gly	Val	Lys	Ala	Ser	Arg	Ser	Tyr	Thr	Phe	Met	Ile	
145					150					155					160	
gtg	ctt	tgg	cct	gtc	ggc	ccc	tat	tat	ggc	gac	gat	cag	ctg	aag	ccg	528
Val	Leu	Ser	Pro	Val	Gly	Ser	Tyr	Tyr	Gly	Asp	Asp	Gln	Leu	Lys	Pro	
				165					170					175		
gtt	aga	atc	tat	gtc	gaa	gat	gag	tat	gtg	agg	gcg	gtc	aac	gga	gga	576
Val	Arg	Ile	Tyr	Val	Glu	Asp	Glu	Tyr	Val	Arg	Ala	Val	Asn	Gly	Gly	
			180					185					190			
gtc	ggg	ttt	gca	aaa	acg	gct	gga	aac	tat	gac	gac	agt	ctt	cag	gca	624
Val	Gly	Phe	Ala	Lys	Thr	Ala	Gly	Asn	Tyr	Ala	Ala	Ser	Leu	Gln	Ala	
		195					200					205				
cag	cgg	aaa	gcg	aat	gaa	ctg	ggc	tat	gac	cag	gta	ctg	tgg	ctg	gac	672
Gln	Arg	Lys	Ala	Asn	Glu	Leu	Gly	Tyr	Asp	Gln	Val	Leu	Trp	Leu	Asp	
	210					215					220					
gac	atc	gaa	aag	aaa	tat	gtg	gaa	gaa	gta	ggg	agc	atg	aac	atc	ttt	720
Ala	Ile	Glu	Lys	Lys	Tyr	Val	Glu	Glu	Val	Gly	Ser	Met	Asn	Ile	Phe	
225					230					235					240	
ttc	gtc	ata	aac	ggg	gaa	gct	gtc	aca	cct	gct	tta	agc	gga	agc	att	768
Phe	Val	Ile	Asn	Gly	Glu	Ala	Val	Thr	Pro	Ala	Leu	Ser	Gly	Ser	Ile	
			245						250					255		
tta	agc	ggg	gtt	aca	cgt	gcg	tct	gcg	att	gaa	ttg	att	cga	agc	tgg	816
Leu	Ser	Gly	Val	Thr	Arg	Ala	Ser	Ala	Ile	Glu	Leu	Ile	Arg	Ser	Trp	
			260				265						270			
ggc	att	ccg	gtt	cgt	gaa	gag	aga	ata	tgg	att	gat	gag	gtg	tat	ggg	864
Gly	Ile	Pro	Val	Arg	Glu	Glu	Arg	Ile	Ser	Ile	Asp	Glu	Val	Tyr	Ala	
		275					280					285				
gac	tct	gca	cgc	gga	gaa	ttg	aca	gag	gtc	ttt	ggc	aca	ggc	acg	gca	912
Ala	Ser	Ala	Arg	Gly	Glu	Leu	Thr	Glu	Val	Phe	Gly	Thr	Gly	Thr	Ala	
	290					295				300						
gca	gtc	ttt	acg	cct	gtc	ggc	gaa	ctc	aac	atc	cat	gga	aaa	acc	gtg	960
Ala	Val	Val	Thr	Pro	Val	Gly	Glu	Leu	Asn	Ile	His	Gly	Lys	Thr	Val	
305					310					315					320	
att	tta	ttt	gac	ttt	tta	atc	ggt	ttt	ctc	tct	aaa	aaa	ctt	tat	tta	1008
Ile	Val	Gly	Asp	Gly	Gln	Ile	Gly	Asp	Leu	Ser	Lys	Lys	Leu	Tyr	Glu	
				325					330						335	
att	tta	ttt	gac	ttt	tta	atc	ggt	ttt	ctc	tct	aaa	aaa	ctt	tat	tta	1056
Ile	Val	Gly	Asp	Gly	Gln	Ile	Gly	Asp	Leu	Ser	Lys	Lys	Leu	Tyr	Glu	
				340					345						350	

Thr Ile Thr Asp Ile Gln Leu Gly Lys Val Lys Gly Pro Phe Asn Trp
 340 345 350

aca gtc gaa gtc tga
 Thr Val Glu Val
 355

1071

<210> 65
 <211> 356
 <212> FRT
 <213> Bacillus subtilis

<400> 65
 Met Asn Lys Leu Ile Glu Arg Glu Lys Thr Val Tyr Tyr Lys Glu Lys
 1 5 10 15

Pro Asp Pro Ser Ser Leu Gly Phe Gly Gln Tyr Phe Thr Asp Tyr Met
 20 25 30

Phe Val Met Asp Tyr Glu Glu Gly Ile Gly Trp His His Pro Arg Ile
 35 40 45

Ala Pro Tyr Ala Pro Leu Thr Leu Asp Pro Ser Ser Ser Val Phe His
 50 55 60

Tyr Gly Gln Ala Val Phe Glu Gly Leu Lys Ala Tyr Arg Thr Asp Asp
 65 70 75 80

Gly Arg Val Leu Leu Phe Arg Pro Asp Gln Asn Ile Lys Arg Leu Asn
 85 90 95

Arg Ser Cys Glu Arg Met Ser Met Pro Pro Leu Asp Glu Glu Leu Val
 100 105 110

Leu Glu Ala Leu Thr Gln Leu Val Glu Leu Glu Lys Asp Trp Val Pro
 115 120 125

Lys Glu Lys Gly Thr Ser Leu Tyr Ile Arg Pro Phe Val Ile Ala Thr
 130 135 140

Glu Pro Ser Leu Gly Val Lys Ala Ser Arg Ser Tyr Thr Phe Met Ile
 145 150 155 160

Val Leu Ser Pro Val Gly Ser Tyr Tyr Gly Asp Asp Gln Leu Lys Pro
 165 170 175

Val Arg Ile Tyr Val Glu Asp Glu Tyr Val Arg Ala Val Asn Gly Gly
 180 185 190

Val Gly Phe Ala Lys Thr Ala Gly Asn Tyr Ala Ala Ser Leu Gln Ala
 195 200 205

Gln Arg Lys Ala Asn Glu Leu Gly Tyr Asp Gln Val Leu Trp Leu Asp
 210 215 220

Ala Ile Ala Lys Lys Tyr Val Gln Glu Val Gly Ser Met Asn Ile Phe
 225 230 235 240

Phe Val Ile Asn Gly Glu Ala Val Thr Pro Ala Leu Ser Gly Ser Ile
 245 250 255

Leu Ser Gly Val Thr Arg Ala Ser Ala Ile Glu Leu Ile Arg Ser Trp
 260 265 270
 Gly Ile Pro Val Arg Glu Glu Arg Ile Ser Ile Asp Glu Val Tyr Ala
 275 280 285
 Ala Ser Ala Arg Gly Glu Leu Thr Glu Val Phe Gly Thr Gly Thr Ala
 290 295 300
 Ala Val Val Thr Pro Val Gly Glu Leu Asn Ile His Gly Lys Thr Val
 305 310 315 320
 Ile Val Gly Asp Gly Gln Ile Gly Asp Leu Ser Lys Lys Leu Tyr Glu
 325 330 335
 Thr Ile Thr Asp Ile Gln Leu Gly Lys Val Lys Gly Pro Phe Asn Trp
 340 345 350
 Thr Val Glu Val
 355

<210> 66
 <211> 1428
 <212> DNA
 <213> Bacillus subtilis

<220>
 <221> CDS
 <222> (1)..(1425)

<400> 66
 atg tta aac ggc caa aaa gaa tat cag gtg gaa aaa gac ttc ctt ggg 48
 Met Leu Asn Gly Gln Lys Glu Tyr Arg Val Glu Lys Asp Phe Leu Gly
 1 5 10 15
 gaa aaa caa att gaa gca gat gtt tat tac gga att cag acg ctc cgt 96
 Glu Lys Gln Ile Glu Ala Asp Val Tyr Tyr Gly Ile Gln Thr Leu Arg
 20 25 30
 gct tct gaa aat ttt ccg atc aca gga tac aaa atc cat gag gaa atg 144
 Ala Ser Glu Asn Phe Pro Ile Thr Gly Tyr Lys Ile His Glu Glu Met
 35 40 45
 att aac gaa ctg gag att ctg aaa aaa gct gaa gct ctt gac aac atg 192
 Ile Asn Ala Leu Ala Ile Val Lys Lys Ala Ala Ala Leu Ala Asn Met
 50 55 60
 gac gtg aaa cgg ctg tat aaa gga att ggc caa gct atc ata caa ggt 240
 Asp Val Lys Arg Leu Tyr Glu Gly Ile Gly Gln Ala Ile Val Gln Ala
 65 70 75
 gct tat tat att ctg aaa ttc ttc ttc ttc gat cat ttt ttc ttc att 288
 Ala Asp Ala Ile Leu Gln Gly Lys Trp His Asp Gln Phe Ile Val Asp
 80 85 90
 ttc att tat ggt ggt ggt aaa att ttc ttc ttc aac att aac att att 336
 Phe Ile Ala Gly Gly Ala Gly Thr Ser Met Asn Met Asn Ala Asn Ala
 95 100 105 110 115

gtt	atc	gga	aac	egg	ggg	ctt	gaa	atc	atg	gga	cat	aaa	aag	gga	gat	384
Val	Ile	Gly	Asn	Arg	Ala	Leu	Glu	Ile	Met	Gly	His	Lys	Lys	Gly	Asp	
		115					120					125				
tat	atc	cat	tta	agt	cca	aac	aca	cat	gtg	aac	atg	tca	cag	tat	cag	432
Tyr	Ile	His	Leu	Ser	Pro	Asn	Thr	His	Val	Asn	Met	Ser	Gln	Ser	Gln	
	130					135					140					
aac	gat	gtg	tta	cgg	act	gat	atc	cat	att	tcc	aca	ttg	aag	ctc	tta	480
Asn	Asp	Val	Phe	Pro	Thr	Ala	Ile	His	Ile	Ser	Thr	Leu	Lys	Leu	Leu	
145				150						155					160	
gaa	aaa	ctg	ctg	aaa	aca	atg	gaa	gat	atg	cat	agt	gtg	ttt	aaa	caa	528
Glu	Lys	Leu	Leu	Lys	Thr	Met	Glu	Asp	Met	His	Ser	Val	Phe	Lys	Gln	
				165				170						175		
aaa	gca	cag	gag	ttt	cac	tct	gtt	att	aaa	atg	ggc	egg	aca	cac	ctt	576
Lys	Ala	Gln	Glu	Phe	His	Ser	Val	Ile	Lys	Met	Gly	Arg	Thr	His	Leu	
			180					185					190			
caa	gat	ggg	gtt	cgg	atc	cgt	ctt	ggc	cag	gaa	tta	gaa	gct	tac	agc	624
Gln	Asp	Ala	Val	Pro	Ile	Arg	Leu	Gly	Gln	Glu	Phe	Glu	Ala	Tyr	Ser	
		195					200					205				
cgt	gtt	ctc	gag	cgt	gat	atc	aaa	cga	atc	aag	caa	tgc	cgc	cag	cac	672
Arg	Val	Leu	Glu	Arg	Asp	Ile	Lys	Arg	Ile	Lys	Gln	Ser	Arg	Gln	His	
	210					215					220					
ctg	tat	gaa	gtc	aac	atg	ggc	gca	act	gct	gtt	ggc	aca	ggg	ctg	aac	720
Leu	Tyr	Glu	Val	Asn	Met	Gly	Ala	Thr	Ala	Val	Gly	Thr	Gly	Leu	Asn	
225					230					235					240	
gct	gat	cct	gaa	tat	atc	aaa	cag	gta	gta	aag	caa	ctt	gct	gat	att	768
Ala	Asp	Pro	Glu	Tyr	Ile	Lys	Gln	Val	Val	Lys	His	Leu	Ala	Asp	Ile	
				245				250						255		
agc	ggg	ctt	cct	ctt	gtc	ggc	gct	gat	cat	ctt	gtt	gat	ggg	aca	caa	816
Ser	Gly	Leu	Pro	Leu	Val	Gly	Ala	Asp	His	Leu	Val	Asp	Ala	Thr	Gln	
			260					265					270			
aat	aca	gat	gac	tat	aca	gag	gta	tca	gct	tca	tta	aaa	gtc	tgc	atg	864
Asn	Thr	Asp	Ala	Tyr	Thr	Glu	Val	Ser	Ala	Ser	Leu	Lys	Val	Cys	Met	
		275					280					285				
atg	aac	atg	tgc	aag	atc	gca	aac	gac	ctg	cac	tta	atg	gag	tgc	gga	912
Met	Asn	Met	Ser	Lys	Ile	Ala	Asn	Asp	Leu	Arg	Leu	Met	Ala	Ser	Gly	
	290					295					300					
cgg	cgc	gac	gga	ctt	ggg	gaa	att	tct	ctg	cct	gca	cgt	cag	cag	ggc	960
Pro	Arg	Ala	Gly	Leu	Ala	Glu	Ile	Ser	Leu	Pro	Ala	Arg	Gln	Pro	Gly	
305					310					315					320	
tca	tct	att	atg	cgg	ggg	aaa	gtc	aat	cgc	gtc	atc					

Ala	Ser	Gln	Ala	Gly	Gln	Leu	Glu	Leu	Asn	Val	Met	Gln	Pro	Val	Leu	
355							360					365				
gtc	ttt	aat	ttg	ott	caa	tcg	atc	agc	atc	atg	aac	aac	ggc	ttc	ogt	1152
Val	Phe	Asn	Leu	Leu	Gln	Ser	Ile	Ser	Ile	Met	Asn	Asn	Gly	Phe	Arg	
370						375					380					
tcg	ttc	act	gac	aac	tgc	tta	aaa	ggc	att	gaa	ggc	aac	gaa	aag	ogt	1200
Ser	Phe	Thr	Asp	Asn	Cys	Leu	Lys	Gly	Ile	Glu	Ala	Asn	Glu	Lys	Arg	
385					390					395					400	
atg	aag	caa	tac	gta	gaa	aaa	agc	gca	ggc	gtg	atc	aca	gct	gtc	aat	1248
Met	Lys	Gln	Tyr	Val	Glu	Lys	Ser	Ala	Gly	Val	Ile	Thr	Ala	Val	Asn	
				405					410					415		
cag	cat	ott	ggg	tat	gaa	ggg	gca	gct	aga	att	ggc	agg	gaa	gca	att	1296
Pro	His	Leu	Gly	Tyr	Glu	Ala	Ala	Ala	Arg	Ile	Ala	Arg	Glu	Ala	Ile	
			420					425					430			
atg	aca	ggg	caa	tct	gtc	ggg	gat	ott	tgt	ctg	cag	cat	gat	gtg	ctg	1344
Met	Thr	Gly	Gln	Ser	Val	Arg	Asp	Leu	Cys	Leu	Gln	His	Asp	Val	Leu	
		435					440					445				
act	gaa	gaa	gaa	ttg	gat	att	att	tta	aac	cca	tat	gag	atg	acc	aaa	1392
Thr	Glu	Glu	Glu	Leu	Asp	Ile	Ile	Leu	Asn	Pro	Tyr	Glu	Met	Thr	Lys	
	450					455				460						
cca	ggt	atc	gca	ggg	aaa	gaa	cta	tta	gaa	aaa	taa					1428
Pro	Gly	Ile	Ala	Gly	Lys	Glu	Leu	Leu	Glu	Lys						
465					470					475						

<210> 67
 <211> 475
 <212> FRT
 <213> Bacillus subtilis

<400> 67
 Met Leu Asn Gly Gln Lys Glu Tyr Arg Val Glu Lys Asp Phe Leu Gly
 1 5 10 15
 Glu Lys Gln Ile Glu Ala Asp Val Tyr Tyr Gly Ile Gln Thr Leu Arg
 20 25 30
 Ala Ser Glu Asn Phe Pro Ile Thr Gly Tyr Lys Ile His Glu Glu Met
 35 40 45
 Ile Asn Ala Leu Ala Ile Val Lys Lys Ala Ala Ala Leu Ala Asn Met
 50 55 60
 Asp Val Lys Arg Leu Tyr Glu Gly Ile Gly Gln Ala Ile Val Gln Ala
 65 70 75 80
 Ala Asp Glu Ile Leu Glu Gly Lys Trp His Asp Gln Phe Ile Val Asp
 85 90 95
 Trp Ile Gln Gly Gly Ala Gly Thr Ser Met Asn Met Asn Ala Asn Trp
 100 105 110 115
 Val Ile Gly Asn Arg Ala Leu Gln Ile Met Gly His Lys Lys Gly Asp
 120 125 130 135

Tyr	Ile	His	Leu	Ser	Pro	Asn	Thr	His	Val	Asn	Met	Ser	Gln	Ser	Gln
130						135					140				
Asn	Asp	Val	Phe	Pro	Thr	Ala	Ile	His	Ile	Ser	Thr	Leu	Lys	Leu	Leu
145					150					155					160
Glu	Lys	Leu	Leu	Lys	Thr	Met	Glu	Asp	Met	His	Ser	Val	Phe	Lys	Gln
				165					170					175	
Lys	Ala	Gln	Glu	Phe	His	Ser	Val	Ile	Lys	Met	Gly	Arg	Thr	His	Leu
			180					185					190		
Gln	Asp	Ala	Val	Pro	Ile	Arg	Leu	Gly	Gln	Glu	Phe	Glu	Ala	Tyr	Ser
		195					200					205			
Arg	Val	Leu	Glu	Arg	Asp	Ile	Lys	Arg	Ile	Lys	Gln	Ser	Arg	Gln	His
	210					215					220				
Leu	Tyr	Glu	Val	Asn	Met	Gly	Ala	Thr	Ala	Val	Gly	Thr	Gly	Leu	Asn
225					230					235					240
Ala	Asp	Pro	Glu	Tyr	Ile	Lys	Gln	Val	Val	Lys	His	Leu	Ala	Asp	Ile
				245					250					255	
Ser	Gly	Leu	Pro	Leu	Val	Gly	Ala	Asp	His	Leu	Val	Asp	Ala	Thr	Gln
			260					265					270		
Asn	Thr	Asp	Ala	Tyr	Thr	Glu	Val	Ser	Ala	Ser	Leu	Lys	Val	Cys	Met
		275					280					285			
Met	Asn	Met	Ser	Lys	Ile	Ala	Asn	Asp	Leu	Arg	Leu	Met	Ala	Ser	Gly
	290					295					300				
Pro	Arg	Ala	Gly	Leu	Ala	Glu	Ile	Ser	Leu	Pro	Ala	Arg	Gln	Pro	Gly
305					310					315					320
Ser	Ser	Ile	Met	Pro	Gly	Lys	Val	Asn	Pro	Val	Met	Ala	Glu	Leu	Ile
				325					330					335	
Asn	Gln	Ile	Ala	Phe	Gln	Val	Ile	Gly	Asn	Asp	Asn	Thr	Ile	Cys	Leu
			340					345					350		
Ala	Ser	Glu	Ala	Gly	Gln	Leu	Glu	Leu	Asn	Val	Met	Glu	Pro	Val	Leu
		355					360					365			
Val	Phe	Asn	Leu	Leu	Gln	Ser	Ile	Ser	Ile	Met	Asn	Asn	Gly	Phe	Arg
	370					375					380				
Ser	Phe	Thr	Asp	Asn	Cys	Leu	Lys	Gly	Ile	Glu	Ala	Asn	Glu	Lys	Arg
385					390					395					400
Met	Lys	Gln	Tyr	Val	Glu	Lys	Ser	Ala	Gly	Val	Ile	Thr	Ala	Val	Asn
				405					410					415	
Pro	His	Leu	Gly	Tyr	Gln	Ala	Ala	Ala	Arg	Ile	Ala	Arg	Ala	Ala	Ile
				420					425					430	
Met	Thr	Gly	Gln	Ser	Val	Arg	Asp	Leu	Lys	Leu	Gln	His	Asp	Val	Leu
		435					440					445			

Thr Glu Glu Glu Leu Asp Ile Ile Leu Asn Pro Tyr Glu Met Thr Lys
450 455 460

Pro Gly Ile Ala Gly Lys Glu Leu Leu Glu Lys
465 470 475

<210> 68

<211> 768

<212> DNA

<213> Bacillus subtilis

<220>

<221> CDS

<222> (1)..(765)

<400> 68

atg aaa cga gaa agc aac att caa gtg ctg agc cgt ggt caa aaa gat 45
Met Lys Arg Glu Ser Asn Ile Gln Val Leu Ser Arg Gly Gln Lys Asp
1 5 10 15

cag cct gtg agc cag att tat caa gta tca aca atg act tct cta tta 96
Gln Pro Val Ser Gln Ile Tyr Gln Val Ser Thr Met Thr Ser Leu Leu
20 25 30

gac gga gta tat gac gga gat ttt gaa ctg tca gag att ccg aaa tat 144
Asp Gly Val Tyr Asp Gly Asp Phe Glu Leu Ser Glu Ile Pro Lys Tyr
35 40 45

gga gac ttc ggt atc gga acc ttt aac aag ctt gac gga gag ctg att 192
Gly Asp Phe Gly Ile Gly Thr Phe Asn Lys Leu Asp Gly Glu Leu Ile
50 55 60

ggg ttt gac ggt gaa ttt tac cgt att agc tca gac gga acc ggc aca 240
Gly Phe Asp Gly Glu Phe Tyr Arg Leu Arg Ser Asp Gly Thr Ala Thr
65 70 75 80

ccg gtc caa aat gga gac cgt tca ccg ttc tgt tca ttt acg ttc ttt 288
Pro Val Gln Asn Gly Asp Arg Ser Pro Phe Cys Ser Phe Thr Phe Phe
85 90 95

aca ccg gac atg acg cac aaa att gat gcg aaa atg aca cgc gaa gac 336
Thr Pro Asp Met Thr His Lys Ile Asp Ala Lys Met Thr Arg Glu Asp
100 105 110

ttt gaa aaa gag atc aac agc atg ctg cca acc aga aar tca ttt tat 384
Phe Glu Lys Glu Ile Asn Ser Met Leu Pro Ser Arg Asn Leu Phe Tyr
115 120 125

gca att cgc att gac gga ttg ttt aaa aat atg gag aca aga aca gta 432
Ala Ile Arg Ile Asp Gly Leu Phe Lys Lys Val Gln Thr Arg Thr Val
130 135 140

aaa ctt caa gaa aaa cct tac tta cca att att gaa cca tta tta aaa 480
Ala Leu Gln Glu Lys Pro Tyr Val Pr Met Val Glu Ala Val Lys Thr
145 150 155 160

taa cca att tta tta tta tac tac tta tta tta tta tta tta tta tta 528
Ala Pr Ile Ile Asn Thr Asp Asn Val Arg Gly Thr Ile Val Gly Phe
165 170 175

ttg aca cca ggt tat gca aac gga atc gcc gtt tct ggc tat cac ctg 676
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 His Phe Ile Asp Glu Gly Arg Asn Ser Gly Gly His Val Phe Asp Tyr
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Gly Phe Asp Gly Glu Phe Tyr Arg Leu Arg Ser Asp Gly Thr Ala Thr
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Tyr Phe Gln Thr Leu Leu Thr Asp Met Leu Glu Ser Gly Lys Ala Thr
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Thr Leu Leu Ala Gly Met Leu Arg Glu Lys Leu Gly Trp Asp Ile Glu
85 90 95

Pro Gln Asn Ile Ala Leu Thr Asn Gly Ser Gln Ser Ala Phe Phe Tyr
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Leu Phe Asn Leu Phe Ala Gly Arg Arg Ala Asp Gly Arg Val Lys Lys
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Val Leu Phe Pro Leu Ala Pro Glu Tyr Ile Gly Tyr Ala Asp Ala Gly
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Pro Glu Gly Gln Phe Lys Tyr His Val Asp Phe Glu His Leu His Ile
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Gly Glu Glu Thr Gly Met Ile Cys Val Ser Arg Pro Thr Asn Pro Thr
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Ile Val Leu Cys Met Ser Leu Ser Lys Leu Gly Leu Pro Gly Ser Arg
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Met Asn Gly Ile Ile Ser Leu Ala Pro Gly Gly Ile Gly Pro Ala Met
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His

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CL11 > 8098

CL12 > RNA

CL13 > Artificial Sequence

CL14 >

CL15 > Description of Artificial Sequence: Full length
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<213> Artificial Sequence

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1111 -

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tat tat tat gga aaa tta gaa tat cac tgg cgt ata gaa aca agc agg 96
Tyr His Asp Gly Lys Leu Glu Tyr His Trp Arg Ile Glu Thr Ser Arg
20 25 30

cat aaa aca gaa gat gag ttt ggg atg att ttg cgg tcc tta ttt gat 144
His Lys Thr Glu Asp Glu Phe Gly Met Ile Leu Arg Ser Leu Phe Asp
35 40 45

cac tcc ggg ctt atg ttt gaa cag ata gat ggc att att att tgg tca 192
His Ser Gly Leu Met Phe Glu Gln Ile Asp Gly Ile Ile Ile Ser Ser
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65 70 75 80

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Phe His Ile Glu Pro Gln Ile Val Gly Pro Gly Met Lys Thr Gly Leu
85 90 95

tat ata aaa tat gat aat ccg aaa gaa gta ggt aca gac aga atc ata 336
Asp Ile Lys Tyr Asp Asn Pro Lys Gln Val Gly Ala Asp Arg Ile Val
100 105 110

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Asp Ala Val Ala Ala Ile His Leu Tyr Gly Asn Pro Leu Ile Val Val
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135 140 145

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His Ser Gly Leu Met Phe Glu Gln Ile Asp Gly Ile Ile Ile Ser Ser
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Val Val Pro Pro Ile Met Phe Ala Leu Glu Arg Met Cys Thr Lys Tyr
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 Tyr Lys Ile Lys Asp Leu Lys Leu Ser Leu Pro Gly Thr Asn Lys Thr
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Val	Ser	Gly	Asp	Gly	Gly	Phe	Leu	Phe	Ser	Ala	Met	Glu	Leu	Glu	Thr	
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gca	ggt	cga	cta	aaa	gca	cca	att	gta	cac	att	gta	tgg	aac	gac	agc	1320
Ala	Val	Arg	Leu	Lys	Ala	Pro	Ile	Val	His	Ile	Val	Trp	Asn	Asp	Ser	
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aca	tat	gac	atg	gtg	aat	tta	tag	aaa	tty	aaa	aaa	tat	aac	ggt	aaa	1360
Thr	Tyr	Asp	Met	Val	His	Phe	Gln	Gln	Leu	Lys	Lys	Tyr	Asn	Arg	Thr	
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tct	ggc	gtc	gat	tta	gga	aat	atc	gat	atc	gtg	aaa	tat	ggc	gaa	agc	1400
Ser	Ala	Val	Asp	Phe	Gly	Asn	Ile	Asp	Ile	Val	Lys	Tyr	Ala	Glu	Ser	
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Phe	Gly	Ala	Thr	Ala	Leu	Arg	Val	Glu	Ser	Pro	Asp	Gln	Leu	Ala	Asp	
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Val	Leu	Arg	Gln	Gly	Met	Asn	Ala	Glu	Gly	Pro	Val	Ile	Ile	Asp	Val	
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ccc	gtt	gac	tac	ggt	gat	aac	att	aat	tta	gca	ggt	gac	aac	att	ccc	1560
Pro	Val	Asp	Tyr	Ser	Asp	Asn	Ile	Asn	Leu	Ala	Ser	Asp	Lys	Leu	Pro	
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<211> 840

<212> 887

<213> Bacillus subtilis

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15

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20

25

30

Gln Gln Phe Met Ala Gln Ala Val Gly Arg Leu Thr Gly Lys Pro Gly

35

40

45

Val Val Leu Val Thr Ser Gly Pro Gly Ala Ser Asn Leu Ala Thr Gly

50

55

60

Leu Leu Thr Ala Asn Thr Gln Gly Arg Pro Val Val Ala Leu Ala Gly

65

70

75

80

Asn Val Ile Arg Ala Tyr Arg Leu Lys Arg Thr His Gln Ser Leu Asp
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 Gly Asp Leu Leu Leu Ala Gln Ala Asp Val Val Leu Thr Ile Gly Tyr
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 Asp Pro Ile Gln Tyr Asp Pro Lys Phe Trp Asn Ile Asn Gly Asp Arg
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 Thr Ile Ile His Leu Asp Gln Ile Ile Ala Asp Ile Asp His Ala Tyr
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 Ser His Ser Ile Trp Met Gln Arg Tyr Phe Arg Ser Tyr Ala Pro Leu
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 Phe Gly Ala Thr Ala Leu Arg Val Glu Ser Pro Asp Gln Leu Ala Asp
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<212> RNA

<213> Artificial Sequence

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binding site

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23

<210> 48

<211> 7

<212> PRT

<213> Artificial Sequence

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<225> Description of Artificial Sequence: 1st
terminus

<400> 48

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<211> 5
 <212> PRT
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 <223> Description of Artificial Sequence: PanC
 C terminus

<400> 90
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<210> 91
 <211> 7
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 <223> Description of Artificial Sequence: PanC
 C terminus

<400> 91
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<210> 92
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 <223> Description of Artificial Sequence: Recombinant
 pAN336 plasmid

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<211> 8503

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Recombinant
pAN004 plasmid

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